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(54) Title: NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE (57) Abstract The invention relates to the identification of members of a gene family from the human respiratory pathogen <i>Chlamydia pneumoniae</i> , encoding surface exposed membrane proteins of a size of approximately 89-101 kDa and of 56-57 kDa, preferably about 89.6-100.3 kDa and about 56.1 kDa. The invention relates to the novel DNA sequences, the deduced amino acid sequences of the corresponding proteins and the use of the DNA sequences and the proteins in diagnosis of infections caused by <i>C. pneumoniae</i> , in pathology, in epidemiology, and as vaccine components.		

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NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE

The present invention relates to the identification of members of a gene family from the human respiratory pathogen *Chlamydia pneumoniae*, encoding surface exposed membrane proteins of a size of approximately 89-101 kDa and of 56-57 kDa, preferably about 89.6-100.3 kDa and about 56.1 kDa. The invention relates to the novel DNA sequences, the deduced amino acid sequences of the corresponding proteins and the use of the DNA sequences and the proteins in diagnosis of infections caused by *C. pneumoniae*, in pathology, in epidemiology, and as vaccine components.

GENERAL BACKGROUND

C. pneumoniae is an obligate intracellular bacteria (Christiansen and Birkelund (1992); Grayston et al. (1986)). It has a cell wall structure as Gram negative bacteria with an outer membrane, a periplasmic space, and a cytoplasmic membrane. It is possible to purify the outer membrane from Gram negative bacteria with the detergent sarkosyl. This fraction is named the 'outer membrane complex (OMC)' (Caldwell et al. (1981)). The COMC (*Chlamydia* outer membrane complex) of *C. pneumoniae* contains four groups of proteins: A high molecular weight protein 98 kDa as determined by SDS-PAGE, a double band of the cysteine rich outer membrane protein 2 (Omp2) protein of 62/60 kDa, the major outer membrane protein (MOMP) of 38 kDa, and the low-molecular weight lipo-protein, Omp3 of 12 kDa. The Omp2/Omp3 and MOMP proteins are present in COMC from all *Chlamydia* species, and these genes have been cloned from both *C. trachomatis*, *C. psittaci* and *C. pneumoniae*. However, the gene encoding 98 kDa protein from *C. pneumoniae* COMC have not been characterized or cloned.

The current state of *C. pneumoniae* serology and detection

C. pneumoniae is an obligate intra-cellular bacteria belonging to the genus *Chlamydia* which can be divided into

four species: *C. trachomatis*, *C. pneumoniae*, *C. psittaci* and *C. pecorum*. Common for the four species is their obligate intra cellular growth, and that they have a biphasic life cycle, with an extracellular infectious particle (the elementary body, EB), and an intercellular replicating form (the reticulate body, RB). In addition the Chlamydia species are characterized by a common lipopolysaccharide (LPS) epitope that is highly immunogenic in human infection. *C. trachomatis* is causing the human ocular infection (trachoma) and genital infections. *C. psittaci* is a variable group of animal pathogens where the avian strains can occasionally infect humans and give rise to a severe pneumonia (ornithosis). The first *C. pneumoniae* isolate was obtained from an eye infection, but it was classified as a non-typable Chlamydia. Under an epidemic outbreak of pneumonia in Finland it was realized that the patients had a positive reaction in the Chlamydia genus specific test, (the lygranum test), and the patients showed a titre increase to the untyped Chlamydia isolates. Similar isolates were obtained in an outbreak of upper respiratory tract infections in Seattle, and the Chlamydia isolates were classified as a new species, *Chlamydia pneumoniae* (Grayston et al. (1989)). In addition, *C. pneumoniae* is suggested to be involved in the development of atherosclerotic lesions and for initiating bronchial asthma (Kuo et al. (1995)). These two conditions are thought to be caused by either chronic infections, by a hypersensitivity reaction, or both.

Diagnosis of *Chlamydia pneumoniae* infections

Diagnosis of acute respiratory tract infection with *C. pneumoniae* is difficult. Cultivation of *C. pneumoniae* from patient samples is insensitive, even when proper tissue culture cells are selected for the isolation. A *C. pneumoniae* specific polymerase chain reaction (PCR) has been developed by Campbell et al. (1992).

Even though *Chlamydia pneumoniae* has in several studies been detected by this PCR it is debated whether this method is suitable for detection under all clinical situations. The reason for this is, that the cells carrying *Chlamydia pneumoniae* in acute respiratory infections have not been determined, and that a chronic carrier state is expected but it is unknown in which organs and cells they are present. Furthermore, the PCR test is difficult to perform due to the low yield of these bacteria and due to the presence of inhibitory substances in the patient samples. Therefore, it will be of great value to develop sensitive and specific sero-diagnostics for detecting both acute and chronic infections. Sero-diagnosis of *Chlamydia* infections is currently based on either genus specific tests as the Lygranum test and ELISA, measuring the antibodies to LPS, or the more species specific tests where antibodies to purified EBs are measured by microimmuno fluorescence (Micro-IF) (Wang et al. (1970)). However, the micro-IF method is read by microscopy, and in order to ensure correct readings the result must be compared to the results with *C. trachomatis* used as antigen due to the cross-reacting antibodies to the common LPS epitope. Thus, there exists in the art an urgent need for development of reliable methods for species specific diagnosis of *Chlamydia pneumoniae*, as has been expressed in Kuop et al. (1995); "...a rapid reliable laboratory test of infection for the clinical laboratory is a major need in the field". Furthermore, the possible involvement of *C. pneumoniae* in atherosclerosis and bronchial asthma clearly warrants the development of an effective vaccine.

DETAILED DISCLOSURE OF THE INVENTION

The present invention aims at providing means for efficient diagnosis of infections with *Chlamydia pneumoniae* as well as the development of effective vaccines against infection with this microorganism. The invention thus relates to species specific diagnostic tests for infection in a mammal, such as a human, with *Chlamydia pneumoniae*, said tests being based on

the detection of antibodies against surface exposed membrane proteins of a size of approximately 89-101 kDa and of 56-57 kDa, preferably of about 89.6-100.3 kDa and about 56.1 kDa (the range in size of the deduced amino acid sequences was from 100.3 to 89.6 except for Omp13 with the size of 56.1 kDa), or the detection of nucleic acid fragments encoding such proteins or variants or subsequences thereof. The invention further relates to the amino acid sequences of proteins according to the invention, to variants and subsequences thereof, and to nucleic acid fragments encoding these proteins or variants or subsequences thereof. The present invention further relates to antibodies against proteins according to the invention. The invention also relates to the use of nucleic acid fragments and proteins according to the invention in diagnosis of *Chlamydia pneumoniae* and vaccines against *Chlamydia pneumoniae*.

Prior to the disclosure of the present invention only a very limited number of genes from *C. pneumoniae* had been sequenced. These were primarily the genes encoding known *C. trachomatis* homologues: MOMP, Omp2, Omp3, Kdo-transferase, the heat shock protein genes GroEl/Es and DnaK, a ribonuclease P homologue and a gene encoding a 76 kDa protein of unknown function. The reason why so few genes have been cloned to date is the very low yield of *C. pneumoniae* which can be obtained after purification from the host cells. After such purification the DNA must be purified from the EBs, and at this step the *C. pneumoniae* DNA can easily be contaminated with host cell DNA. In addition to these inherent difficulties, it is exceedingly difficult to cultivate *C. pneumoniae* and use DNA technology to produce expression libraries with very low amounts (few μ g) of DNA. It has been known since 1993 (Melgosa et al., 1993) that a 98 kDa protein is present in OMC from *C. pneumoniae*. Even though the protein bands of 98 kDa was mentioned to be part of the OMC of *C. pneumoniae* by Melgosa, the gene sequences and thus the deduced amino acid sequences have not been determined. Only

bands originating from *Chlamydia pneumoniae* proteins in general separated by SDS-PAGE are describe therein. However, the gene encoding this protein has not been determined before the present invention. Only a very weak or
5 no reaction with patient sera can be observed to the 98 kDa protein (Campbell et al. 1990) and prior to the work of the present inventors it has not been recognized that the 89-101 kDa proteins are surface exposed or that they in fact is immunogenic. In this report it is described that a number of
10 human serum samples reacts with a *C. pneumoniae* protein that in SDS-PAGE migrate as 98 kDa. The protein was not further characterized and it is therefore not in conflict with the present application.

Halme et al. (1997) described the presence of human T-cell
15 epitopes in *C. pneumoniae* proteins of 92-98 kDa. The proteins were eluted from SDS-PAGE of total chlamydia proteins but the identity of the proteins were not determined.

Use of antibodies to screen expression libraries is a well known method to clone fragments of genes encoding antigenic
20 parts of proteins. However, since patient sera do not show a significant reaction with the 98 kDa protein it has not been possible to use patient serum to clone the proteins.

It was known that monoclonal antibodies generated by the
25 inventors reacted with conformational epitopes on the surface of *C. pneumoniae* and that they also reacted with *C. pneumoniae* OMC by immuno-electron microscopy (Christiansen et al. 1994). Furthermore, the 98 kDa protein is the only unknown protein from the *C. pneumoniae* OMC (Melgosa et al.
30 1993). The present inventors chose to take an unconventional step in order to clone the gene encoding the hitherto unknown 98 kDa protein: *C. pneumoniae* OMC was purified and the highly immunogenic conformational epitopes were destroyed by SDS-treatment of the antigen before immunization. Thereby an
35 antibody (PAB 150) to less immunogenic linear epitopes was obtained. This provided the possibility to obtain an

antiserum which could detect the protein, and it was shown that a gene family encoding the 89-101 kDa and 56 proteins according to the invention could be detected in colony blotting of recombinant *E. coli*.

5 Mice infected with *C. pneumoniae* generate antibodies to the proteins identified by the inventors and named Omp4-15, but do not recognize the SDS treated heat denatured antigens normally used for SDS-PAGE and immunoblotting. However, a strong reaction was seen if the antigen was not heat
10 denatured. It is therefore highly likely that if a similar reaction is seen in connection with human infections the antigens of the present invention will be of invaluable use in sero-diagnostic tests and may very likely be used as a vaccine for the prevention of infections.

15

By generating antibodies against COMC from *C. pneumoniae* a polyclonal antibody (PAB 150) was obtained which reacted with all the proteins. This antibody was used to identify the genes encoding the 89.6-101.3 kDa and 56.1 kDa proteins in an
20 expression library of *C. pneumoniae* DNA. A problem in connection with the present invention was that a family comprising a number of similar genes were found in *C. pneumoniae*. Therefore, a large number of different clones were required to identify clusters of fragments. Only because
25 the rabbit antibody generated by the use of SDS-denatured antigens contained antibodies to a high number of different epitopes positioned on different members of the protein family did the inventors succeed in cloning and sequencing four of the genes. One gene was fully sequenced, a second was
30 sequenced except for the distal part and shorter fragments of two additional genes were obtained by this procedure. To obtain the DNA sequence of the additional genes and to search for more members of the gene family long range PCR with primers derived from the sequenced genes, and primers from
35 the genes already published in the database were used. This approach gave rise to the detection of additional eight genes belonging to this family. The genes were situated in two gene

clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the second. Full sequence was obtained from Omp4,5,6,7,8,9,10,11 and 13, and partial sequence of Omp12,14. Omp13 was a truncated gene of 1545 nucleotides. The rest of the full length genes were from 2526 (Omp7) to 2838 (Omp15) nucleotides. The deduced amino acid sequences revealed putative polypeptides of 89.6 to 100.3 kDa, except for Omp13 of 56.1 kDa. Alignment of the deduced amino acid sequences showed a maximum identity of 49% (Omp5/Omp9) when all the sequences were compared. Except for Omp13, the lowest homology was to Omp7 with no more than 34% identity to any of the other amino acid sequences. The scores for Omp13 was from 29-32% to all the other sequences.

In the present context SEQ ID Nos. 1 and 2 correspond to Omp4, SEQ ID Nos 3 and 4 correspond to Omp5, SEQ ID Nos 5 and 6 correspond to Omp6, SEQ ID Nos 7 and 8 correspond to Omp7, SEQ ID Nos 9 and 10 correspond to Omp8, SEQ ID Nos 11 and 12 correspond to Omp9, SEQ ID Nos 13 and 14 corresponds to Omp10, SEQ ID Nos 15 and 16 corresponds to Omp11, SEQ ID Nos 17 and 18 corresponds to Omp12, SEQ ID Nos 19 and 20 corresponds to Omp13, SEQ ID Nos 21 and 22 corresponds to Omp14, and SEQ ID Nos 23 and 24 corresponds to Omp15.

The estimated size of the Omp proteins of the of the present invention are listed in the following. Omp 4 has a size of 98.9 kDa, Omp5 has an estimated size of 97.2 kDa, Omp6 has an estimated size of 100.3 kDa, Omp7 has an estimated size of 89.7 kDa, Omp8 has an estimated size of 90.0 kDa, Omp9 has an estimated size of 96.7 kDa, Omp10 has an estimated size of 98.4 kDa, Omp11 has an estimated size of 97.6 kDa, Omp13 has an estimated size of 56.1 kDa, Omp 12 and 14 being partial.

Furthermore, SEQ ID No 25 is a subsequence of SEQ ID No 3, SEQ ID No 26 is a subsequence of SEQ ID No 4, SEQ ID No 27 is a subsequence of SEQ ID No 5, SEQ ID No 28 is a subsequence of SEQ ID No 6, SEQ ID No 29 is a subsequence of SEQ ID No 7, and SEQ ID No 30 is a subsequence of SEQ ID No 8.

Part of the omp proteins were expressed as fusion proteins, and mice polyclonal monospecific antibodies against the proteins were produced. The antibodies reacted with the surface of *C. pneumoniae* in both immunofluorescence and
5 immunoelectron microscopy. This shows for the first time that the 89-101 kDa and 56-57 kDa protein family in *C. pneumoniae* comprises surface exposed outer membrane proteins. This important finding leads to the realization that members of
10 the 89-101 kDa and 56-57 kDa *C. pneumoniae* protein family are good candidates for the development of a sero diagnostic test for *C. pneumoniae*, as well as the development of a vaccine against infections with *C. pneumoniae* based on using these proteins. Furthermore, the proteins may be used as
15 epidemiological markers, and polyclonal monospecific sera against the proteins can be used to detect *C. pneumoniae* in human tissue or detect *C. pneumoniae* isolates in tissue culture. Also, the genes encoding the 89-101 kDa and 56-57 kDa such as the 89.6-100.3 kDa and 56.1 protein family may be used for the development of a species specific diagnostic
20 test based on nucleic acid detection/amplification.

The full length Omp4 was cloned into an expression vector system that allowed expression of the Omp4 polypeptide. This polypeptide was used as antigen for immunization of a rabbit. Since the protein was purified under denaturing condition the
25 antibody did not react with the native surface of *C. pneumoniae*, but it reacted with a 98 kDa protein in immunoblotting where purified *C. pneumoniae* EB was used as antigen. Furthermore, the antibody reacted in paraffin embedded sections of lung tissue from experimentally infected
30 mice.

A broad aspect of the present invention relates to a species specific diagnostic test for infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said test comprising
35 detecting in a patient or preferable in a patient sample the presence of antibodies against proteins from the outer membrane of *Chlamydia pneumoniae*, said proteins being of a

molecular weight of 89-101 kDa or 56-57 kDa, or detecting the presence of nucleic acid fragments encoding said outer membrane proteins or fragments thereof.

5 In the context of the present application, the term "patient sample" should be taken to mean an amount of serum from a patient, such as a human patient, or an amount of plasma from said patient, or an amount of mucosa from said patient, or an amount of tissue from said patient, or an amount of
10 expectorate, forced sputum or a bronchial aspirate, an amount of urine from said patient, or an amount of cerebrospinal fluid from said patient, or an amount of atherosclerotic lesion from said patient, or an amount of mucosal swaps from said patient, or an amount of cells from a tissue culture
15 originating from said patient, or an amount of material which in any way originates from said patient. The in vivo test in a human according to the present invention includes a skin test known in the art such as an intradermal test, e.g. similar to a Mantoux test. In certain patients being very
20 sensitive to the test, such as is often the case with children, the test could be non-invasive, such as a superficial test on the skin, e.g. by use of a plaster

In the present context, the term 89-101 kDa protein means proteins normally present in the outer membrane of *Chlamydia*
25 *pneumoniae*, which in SDS-PAGE can be observed as one or more bands with an apparent molecular weight substantially in the range of 89-101 kDa. From the deduced amino acid sequences the molecular size varies from 89.6 to 100.3 kDa.

Within the scope of the present invention are species
30 specific sero-diagnostic tests based on the usage of the genes belonging to the gene family disclosed in the present application.

Preferred embodiments of the present invention relate to species specific diagnostic tests according to the invention,
35 wherein the outer membrane proteins have sequences selected

from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24.

5 When used in connection with proteins according to the present invention the term "variant" should be understood as a sequence of amino acids which shows a sequence similarity of less than 100% to one of the proteins of the invention. A
10 variant sequence can be of the same size or it can be of a different size as the sequence it is compared to. A variant will typically show a sequence similarity of preferably at least 50%, preferably at least 60%, more preferably at least 70%, such as at least 80%, e.g. at least 90%, 95% or 98%.

The term "sequence similarity" in connection with sequences
15 of proteins of the invention means the percentage of identical and conservatively changed amino acid residues (with respect to both position and type) in the proteins of the invention and an aligned protein of equal or different length. The term "sequence identity" in connection with
20 sequences of proteins of the invention means the percentage of identical amino acid with respect to both position and type in the proteins of the invention and an aligned protein of equal or different length.

Within the scope of the present invention are subsequences of
25 one of the proteins of the invention, meaning a consecutive stretch of amino acid residues taken from SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24. A subsequence will
30 typically comprise at least 100 amino acids, preferably at least 80 amino acids, more preferably at least 70 amino acids, such as 50 amino acids. It might even be as small as 10-50 amino acids, such as 20-40 amino acids, e.g. about 30 amino acids. A subsequence will typically show a sequence
35 homology of at least 50%, preferably at least 60%, more

preferably at least 70%, such as at least 80%, e.g. at least 90%, 95% or 98%.

Diagnostic tests according to the invention include immunoassays selected from the group consisting of a direct
5 or indirect EIA such as an ELISA, an immunoblot technique such as a Western blot, a radio immuno assay, and any other non-enzyme linked antibody binding assay or procedure such as a fluorescence, agglutination or precipitation reaction, and nephelometry.

- 10 A preferred embodiment of the present invention relates to species specific diagnostic tests according to the invention, said test comprising an ELISA, wherein antibodies against the proteins of the invention or fragments thereof are detected in samples.
- 15 A preferred embodiment of the invention, is an ELISA based on detection in samples of antibodies against proteins of the invention. The ELISA may use proteins of the invention, or variants thereof, i.e. the antigen, as coating agent. An ELISA will typically be developed according to standard
20 methods well known in the art, such as methods described in "Antibodies; a laboratory manual", Ed. David Lane Harlow, Cold Spring Harbor laboratories (1988), which is hereby incorporated by reference.

- Recombinant proteins will be produced using DNA sequences
25 obtained essentially using methods described in the examples below. Such DNA sequences, comprising the entire coding region of each gene in the gene family of the invention, will be cloned into an expression vector from which the deduced protein sequence can be purified. The purified proteins will
30 be analyzed for reactivity in ELISA using both monoclonal and polyclonal antibodies as well as sera from experimentally infected mice and human patient sera.

From the experimentally infected mice sera it is known that non-linear epitopes are recognized predominantly. Thus, it is contemplated that different forms of purification schemes known in the art will be used to analyze for the presence of discontinuous epitopes, and to analyze whether the human immune response is also directed against such epitopes.

Preferred embodiments of the present invention relate to species specific diagnostic tests according to the invention, wherein the nucleic acid fragments have sequences selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, and SEQ ID NO: 23.

In connection with nucleic acid fragments according to the present invention the term "variant" should be understood as a sequence of nucleic acids which shows a sequence homology of less than 100%. A variant sequence can be of the same size or it can be of a different size as the sequence it is compared to. A variant will typically show a sequence homology of at least 50%, preferably at least 60%, more preferably at least 70%, such as at least 80%, e.g. at least 90%, 95% or 98%.

The term "sequence homology" in connection with nucleic acid fragments of the invention means the percentage of matching nucleic acids (with respect to both position and type) in the nucleic acid fragments of the invention and an aligned nucleic acid fragment of equal or different length.

In order to obtain information concerning the general distribution of each of the genes according to the present invention, PCR will be performed for each gene on all available *C. pneumoniae* isolates. This will provide information on the general variability of the genes or nucleic acid fragments of the invention. Variable regions will be sequenced. From patient samples PCR will be used to

amplify variable parts of the genes for epidemiology. Non-variable parts will be used for amplification by PCR and analyzed for possible use as a diagnostic test. It is contemplated that if variability is discovered, PCR of variable regions can be used for epidemiology. PCR of non-variable regions can be used as a species specific diagnostic test. Using genes encoding proteins known to be invariable in all known isolates prepared as targets for PCR to genes encoding proteins with unknown function.

- 10 Particularly preferred embodiments of the present invention, relate to diagnostic tests according to the invention, wherein detection of nucleic acid fragments is obtained by using nucleic acid amplification, preferably polymerase chain reaction (PCR).
- 15 Within the scope of the present invention is a PCR based test directed at detecting nucleic acid fragments of the invention or variants thereof. A PCR test will typically be developed according to methods well known in the art and will typically comprise a PCR test capable of detecting and differentiating
- 20 between nucleic acid fragments of the invention. Preferred are quantitative competitive PCR tests or nested PCR tests. The PCR test according to the invention will typically be developed according to methods described in detail in EP B 540 588, EP A 586 112, EP A 643 140 OR EP A 669 401, which
- 25 are hereby incorporated by reference.

Within the scope of the present invention are variants and subsequences of one of the nucleic acid fragments of the invention, meaning a consecutive stretch of nucleic acids taken from SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID

30 NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 19, SEQ ID NO: 21, or SEQ ID NO: 23. A variant or subsequence will preferably comprise at least 100 nucleic acids, preferably at least 80 nucleic acids, more preferably at least 70 nucleic acids, such as at least 50 nucleic acids.

35 It might even be as small as 10-50 nucleic acids, such as

20-40 nucleic acids, e.g. about 30 nucleic acids. A subsequence will typically show a sequence homology of at least 30%, preferably at least 60%, more preferably at least 70%, such as at least 80%, e.g. at least 90%, 95% or 98%. The shorter the subsequence, the higher the required homology. Accordingly, a subsequence of 100 nucleic acids or lower must show a homology of at least 80%.

A very important aspect of the present invention relates to proteins of the invention derived from *Chlamydia pneumoniae* having amino acid sequences selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24 having a sequence similarity of at least 50%, preferably at least 60%, more preferably at least 70%, such as at least 80%, e.g. at least 90%, 95% or 98% and a similar biological function.

By the term "similar biological function" is meant that the protein shows characteristics similar with the proteins derivable from the membrane proteins of *Chlamydia pneumoniae*. Such proteins comprise repeated motifs of GGAI (at least 2, preferable at least 3 repeats) and/or conserved positions of tryptophan, (w).

Comparison of the DNA sequences from genes encoding Omp4-15 shows that the overall similarity between the individual genes ranges between 43-55%. Comparison of the amino acid sequences of Omp4-15 shows 34-49% identity and 53-64% similarity. The homology is generally scattered along the entire length of the deduced amino acids. However, as seen from figure 8 A - J there are some regions in which the homology is more pronounced. This is seen in the repeated sequence where the sequence GGAI is repeated 4-7 times in the genes. It is interesting that the DNA homology is not conserved for the sequences encoding the four amino acids GGAI. This may indicate a functional role of this part of the

protein and indicates that the repeated structure did not occur by a duplication of the gene. In addition to the four amino acid repeats GGAI a region from amino acid 400 to 490 has a higher degree of homology than the rest of the protein, with the conserved sequence FYDPI occurring in all sequences. As further indication of similarity in function the amino acid tryptophan (W) is perfectly conserved at 4-6 localizations in the C-terminal part of the protein.

Since none of the genes and deduced amino acid sequences of the invention are identical the following is within the scope of the present invention; production of monospecific antibodies, the use of said antibodies for characterizing which *C. pneumoniae* proteins are expressed, the use of said antibodies for characterizing at which time during developmental life cycle said *C. pneumoniae* proteins are expressed, and the use of said antibodies for characterizing the precise cellular localization of said *C. pneumoniae* proteins. Also within the scope of the present invention is the use of monospecific antibodies against proteins of the invention for determining which part of said proteins is surface exposed and how proteins in the *C. pneumoniae* COMC interact with each other.

Preferred embodiments of the present invention relate to polypeptides which comprise subsequences of the proteins of the invention, said subsequences comprising the sequence GGAI. Further preferred embodiments of the present invention relate to polypeptides which comprise subsequences of the proteins of the invention, said subsequences comprising the sequence FSGE.

Polypeptides according to the invention will typically be of a length of at least 6 amino acids, preferably at least 15 amino acids, preferably at least 20 amino acids, preferably at least 25 amino acids, preferably at least 30 amino acids, preferably at least 35 amino acids, preferably at least 40 amino acids, preferably at least 45 amino acids, preferably

at least 50 amino acids, preferably at least 55 amino acids, preferably at least 100 amino acids.

A very important aspect of the present invention relates to nucleic acid fragments of the invention derived from

5 *Chlamydia pneumoniae*, variants and subsequences thereof.

Another important aspect of the present invention relates to antibodies against the proteins according to the invention, such antibodies including polyclonal monospecific antibodies and monoclonal antibodies against proteins with sequences

10 selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24.

A very important aspect of the present invention relates to diagnostic kits for the diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said kits comprising one or more proteins with amino acid sequences

15 selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24.

Another very important aspect of the present invention relates to diagnostic kits for the diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said kits comprising antibodies against a protein with an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24.

25 Antibodies included in a diagnostic kit according to the invention can be polyclonal or monoclonal or a mixture hereof.

Still another very important aspect of the present invention relates to diagnostic kits for the diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said kits comprising one or more nucleic acid fragments with

5 sequences selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, and SEQ ID NO: 23.

10 An aspect of the present invention relates to a composition for immunizing a mammal, such as a human, against *Chlamydia pneumoniae*, said composition comprising one or more proteins with amino acid sequences selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, 15 SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24.

An important role for the proteins of the invention in prevention of infection of a mammal, such as a human, with *C. pneumoniae* is expected. Thus proteins of the invention, 20 including variants and subsequences will be produced, typically by using recombinant techniques, and will then be used as an antigen in immunization of mammals, such as rabbits. Subsequently, the hyper immune sera obtained by the immunization will be analyzed for protection against *C. pneumoniae* infection using a tissue culture assay. In 25 addition it is contemplated that monoclonal antibodies will be produced, typically using standard hybridoma techniques, and analyzed for protection against infection with *C. pneumoniae*.

30 It is envisioned that particularly interesting and immunogenic epitopes will be found in connection with the proteins of the invention, which will comprise subsequences of said proteins. It is preferred to use polypeptides comprising such subsequences of the proteins of the invention

in immunizing a mammal, such as a human, against *Chlamydia pneumoniae*.

An important aspect of the present invention relates to the use of proteins with sequences selected from the group

5 consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24 in diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*.

10 A preferred embodiment of the present invention relates to the use of proteins according to the invention in an undenatured form, in diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*.

A very important aspect of the present invention relates to
15 the use of proteins with sequences selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, and SEQ ID NO: 24, for immunizing a mammal, such as a human, against
20 *Chlamydia pneumoniae*.

A preferred embodiment of the present invention relates to the use of proteins according to the invention in an undenatured form, for immunizing a mammal, such as a human, against *Chlamydia pneumoniae*.

25 A very important aspect of the present invention relates to the use of nucleic acid fragments with nucleotide sequences selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO:
30 19, SEQ ID NO: 21, and SEQ ID NO: 23 for immunizing a mammal, such as a human, against *Chlamydia pneumoniae*.

It is envisioned that one type of vaccine against *C. pneumoniae* will be developed by using gene-gun vaccination of mice. Typically, different genetic constructs containing nucleic acid fragments, combinations of nucleic acid fragments according to the invention will be used in the gene-gun approach. The mice will then subsequently be analyzed for production of both humoral and cellular immune response and for protection against infection with *C. pneumoniae* after challenge herewith.

- 10 In line with this, the invention also relates to the uses of the proteins of the invention as a pharmaceutical (a vaccine) as well as to the uses thereof for the preparation of a vaccine against infections with *Chlamydia pneumoniae*.

- Preparation of vaccines which contain protein sequences as active ingredients is generally well understood in the art, as exemplified by U.S. Patents 4,608,251; 4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4,578,770, all incorporated herein by reference. Typically, such vaccines are prepared as injectables either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants which enhance the effectiveness of the vaccines.

- The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. These compositions take the form of

solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10-95% of active ingredient, preferably 25-70%, and optionally a suitable carrier.

- 5 The protein sequences may be formulated into the vaccine as neutral or salt forms known in the art. The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered
10 depends on the subject to be treated. Suitable dosage ranges are of the order of several hundred micrograms active ingredient per vaccination with a preferred range from about 0.1 μ g to 1000 μ g. The immune response may be enhanced if the vaccine further comprises an adjuvant substance as known in
15 the art. Other possibilities involve the use of immunomodulating substances such as lymphokines (e.g. IFN- γ , IL-2 and IL-12) or synthetic IFN- γ inducers such as poly I:C in combination with the above-mentioned adjuvants.

- It is also possible to produce a living vaccine by introducing, into a non-pathogenic microorganism, at least one
20 nucleic acid fragment encoding a protein fragment or protein of the invention, and effecting expression of the protein fragment or the protein on the surface of the microorganism (e.g. in the form of a fusion protein including a membrane
25 anchoring part or in the form of a slightly modified protein or protein fragment carrying a lipidation signal which allows anchoring in the membrane). The skilled person will know how to adapt relevant expression systems for this purpose.

- Another part of the invention is based on the fact that
30 recent research have revealed that a DNA fragment cloned in a vector which is non-replicative in eukaryotic cells may be introduced into an animal (including a human being) by e.g. intramuscular injection or percutaneous administration (the so-called "gene gun" approach). The DNA is taken up by e.g.
35 muscle cells and the gene of interest is expressed by a

promoter which is functioning in eukaryotes, e.g. a viral promoter, and the gene product thereafter stimulates the immune system. These newly discovered methods are reviewed in Ulmer et al., 1993, which hereby is included by reference.

- 5 Thus, a nucleic acid fragment encoding a protein or protein of the invention may be used for effecting *in vivo* expression of antigens, i.e. the nucleic acid fragments may be used in so-called DNA vaccines. Hence, the invention also relates to a vaccine comprising a nucleic acid fragment encoding a
10 protein fragment or a protein of the invention, the vaccine effecting *in vivo* expression of antigen by an mammal, such as a human, to whom the vaccine has been administered, the amount of expressed antigen being effective to confer substantially increased resistance to infections with
15 *Chlamydia pneumoniae* in an mammal, such as a human.

- The efficacy of such a "DNA vaccine" can possibly be enhanced by administering the gene encoding the expression product together with a DNA fragment encoding a protein which has the capability of modulating an immune response. For instance, a
20 gene encoding lymphokine precursors or lymphokines (e.g. IFN- γ , IL-2, or IL-12) could be administered together with the gene encoding the immunogenic protein fragment or protein, either by administering two separate DNA fragments or by administering both DNA fragments included in the same vector.
25 It is also a possibility to administer DNA fragments comprising a multitude of nucleotide sequences which each encode relevant epitopes of the protein fragments and proteins disclosed herein so as to effect a continuous sensitization of the immune system with a broad spectrum of these epitopes.
- 30 The following experimental non-limiting examples are intended to illustrate certain features and embodiments of the invention.

LEGENDS TO FIGURES

Figure 1. The figure shows electron microscopy of negative stained purified *C. pneumoniae* EB (A) and purified OMC (B).

5 Figure 2. The figure shows silver stained 15% SDS-PAGE of purified EB and OMC. Lane 1, purified *C. pneumoniae* EB; lane 2, *C. pneumoniae* OMC; lane 3, purified *C. trachomatis* EB; and lane 4 *C. trachomatis* OMC.

10 Figure 3. The figure shows immunoblotting of *C. pneumoniae* EB separated by 10% SDS-PAGE, transferred to nitrocellulose and reacted with rabbit anti *C. pneumoniae* OMC.

Figure 4. The figure shows coomassie blue stained 7.5% SDS-PAGE of recombinant pEX that were detected by the rabbit anti *C. pneumoniae* serum. Arrow indicated the localization of the 117 kDa b-galactosidase protein.

15 Figure 5. The figure shows immunoblotting of recombinant pEX clones detected by colony blotting separated by 7.5% SDS-PAGE and transferred to nitrocellulose and reacted with rabbit anti *C. pneumoniae* OMC. Lane 1, seablue molecular weight standard. Lane 2-6 pEX clones cultivated at 42°C to
20 induce the production of the b-galactosidase fusion proteins.

Figure 6. The figure shows sequence strategy for Omp4 and Omp5. Arrows indicates primers used for sequencing.

25 Figure 7. *C. pneumoniae* omp genes. The genes are arranged in two clusters. In cluster 1 Omp12, 11, 10, 5, 4, 13, and 14 are found. In cluster 2 are found Omp6, 7, 8, 9, and 15.

Figure 8 A - J. The figure shows alignment of *C. pneumoniae* Omp4-15, using the program pileup in the GCG package.

Figure 9. The figure shows immunofluorescence of *C. pneumoniae* infected HeLa, 72 hrs. after infection, reacted

with mouse monospecific anti-serum against pEX3-36 fusion protein. pEX3-36 is a part of the Omp5 gene.

Figure 10. The figure shows immunoblotting of *C. pneumoniae* EB, lane 1-3 heated to 100°C in SDS-sample buffer, lane 4-6 unheated. Lane 1 reacted with rabbit anti *C. pneumoniae* OMC; lane 2 and 4 pre-serum; lane 3 and 5 polyclonal rabbit anti pEX1-1 fusion protein; lane 6 MAb 26.1.

Figure 11. The figure shows immunoblotting of *C. pneumoniae* EB, lane 1-4 heated to 100°C in SDS-sample buffer, lane 5-6 unheated. Reacted with serum from C57-black mice 14 days after infection with 10^7 CFU of *C. pneumoniae*. Lane 1 and 5 mouse 1; lane 2 and 6 mouse 2; lane 3 and 5 mouse 3; and lane 4 and 8 mouse 4.

Figure 12. The figure shows immunohistochemistry analysis of mouse lung tissue with *C. pneumoniae* inclusions present both in the bronchial epithelium and in the lung parenchyma (arrows).

EXAMPLE 1

Cloning of the genes encoding the 98/95 kDa *C. pneumoniae* COMC proteinsPurification of *C. pneumoniae* EBs and COMC

5 *C. pneumoniae* was cultivated in HeLa cells. Cultivation was done according to the specifications of Miyashita and Matsumoto (1992), with the modification that centrifugation of supernatant and of the later precipitate and turbid bottom layer was carried out at 100,000 X g. The microorganism
10 attached to the HeLa cells by 30 minutes of centrifugation at 1000 x g, after which the cells were incubated in RPMI 1640 medium (Gibco BRL, Germany cat No. 51800-27), containing 5% foetal calf serum (FCS, Gibco BRL, Germany Cat No. 10106.169) gentamicin for two hours at 37°C in 5% CO₂ atmosphere. The
15 medium was changed to medium that in addition contained 1 mg per ml of cycloheximide. After 48 hours of incubation a coverslip was removed from the cultures and the inclusion was tested with an antibody specific for *C. pneumoniae* (MAb 26.1) (Christiansen et al. 1994) and a monoclonal antibody specific
20 for the species *C. trachomatis* (MAb 32.3, Loke diagnostics, Århus Denmark) to ensure that no contamination with *C. trachomatis* had occurred. The HeLa cells were tested by Hoechst stain for Mycoplasma contamination as well as by culture in BEa and BEg medium (Freund et al., 1979). Also the
25 *C. pneumoniae* stocks were also tested for Mycoplasma contamination by cultivation in BEa and BEg medium. No contamination with *C. trachomatis*, Mycoplasmas or bacteria were detected in cultures or cells. 72 hours post-infection the monolayer was washed in PBS, the cells were loosened in
30 PBS with a rubber policeman, and the Chlamydia were liberated from the host cell by sonication. The *C. pneumoniae* EBs and RBs were purified on discontinuous density gradients (Miyashita et al. (1992)). The purity of the Chlamydia EBs were verified by negative staining and electronmicroscopy
35 (Figure 1), only particles of a size of 0.3 to 0.5 mm were

detected in agreement with the structure of *C. pneumonia* EBs. The purified Chlamydia EBs were subjected to sarkosyl extraction as described by Caldwell et al (1981) with the modification that a brief sonication was used to suspend the COMC. The purified COMC was tested by electronmicroscopy and negative staining (Figure 1), where a folded outer membrane complex was seen.

SDS-PAGE analysis of purified EBs and COMC

The proteins from purified EBs and *C. pneumoniae* OMC were separated on 15% SDS-polyacrylamide gel, and the gel was silver stained (Figure 2), in lane 1 it is seen that the purified EBs contain major proteins of 100/95 kDa and a protein of 38 kDa, in the purified COMC (lane 2) these two protein groups are also dominant. In addition, proteins with a molecular weight of 62/60 kDa, 55 kDa, and 12 kDa have been enriched in the COMC preparation. When the purified *C. pneumoniae* EBs are compared to purified *C. trachomatis* EB (lane 3) it is seen that predominant protein in the *C. trachomatis* EB is the major outer membrane protein (MOMP), and it is also the dominant band in the COMC preparation of *C. trachomatis* (lane 4), and Omp2 of 60/62 kDa as well as Omp3 at 12 kDa are seen in the preparation. However, no major bands with a size of 100/95 kDa are detected as in the *C. pneumoniae* COMC preparation.

Production of rabbit polyclonal antibodies against *C. pneumoniae* COMC

To ensure production of rabbit antibodies that would recognize all the *C. pneumoniae* proteins in immuno-blotting and colony-blotting 10 µg of COMC antigen was dissolved in 20 µl of SDS sample buffer and thereafter divided into 5 vials. The dissolved antigen was further diluted in one ml of PBS and one ml of Freund incomplete adjuvant (Difco laboratories, USA cat. No. 0639-60-6) and injected into the quadriceps muscle of a New Zealand white rabbit. The rabbit was given:

three times intramuscular injections at an interval of one week, and after further three weeks the dissolved COMC protein, diluted in one ml PBS was injected intravenously, and the procedure was repeated two weeks later. Eleven weeks after the beginning of the immunization, the serum was obtained from the rabbit. Purified *C. pneumoniae* EBs were separated by SDS-PAGE, and the proteins were electrotransferred to nitrocellulose membrane. The membrane was blocked and immunostained with the polyclonal COMC antibody (Figure 3). The serum recognized proteins with a size of 100/95, 60 and 38 kDa in the EB preparation. This is in agreement with the sizes of the outer membrane proteins.

Cloning of the COMC proteins

Due to the cultivation of *C. pneumoniae* in HeLa cells, contaminating host cell DNA could be present in the EB preparations. Therefore, the purified EB preparations were treated with DNase to remove contaminating DNA. The *C. pneumoniae* DNA was then purified by CsCl gradient centrifugation. The *C. pneumoniae* DNA was partially digested with Sau3A and the fractions containing DNA fragments with a size of approx. 0.5 to 4.0 kb were cloned into the expression vector system pEX (Boehringer, Germany cat. No. 1034 766, 1034 774, 1034 782). The pEX vector system has a β -galactosidase gene with multiple cloning sites in the 3' end of the β -galactosidase gene. Expression of the gene is regulated by the PR promoter, so the protein expression can be induced by elevating the temperature from 32 to 42°C. The colonies of recombinant bacteria were transferred to nitrocellulose membranes, and the temperature was increased to 42°C for two hours. The bacteria were lysed by placing the nitrocellulose membranes on filters soaked in 5% SDS. The colonies expressing outer membrane proteins were detected with the polyclonal antibody raised against *C. pneumoniae* COMC. The positive clones were cultivated in suspension and induced at 42°C for two hours. The protein profile of the clones were analysed by SDS-PAGE, and increases in the size

of the induced b-galactosidase were observed (Figure 4). In addition, the proteins were electrotransferred to nitrocellulose membranes, and the reaction with the polyclonal serum against COMC was confirmed (Figure 5).

5 Sequencing of positive COMC clones

To characterize the pEX clones, the inserted *C. pneumoniae* DNA was sequenced. The resulting DNA sequences were searched against the prokaryotic sequences in the GenEmbl database. The search identified 6 clones as part of the Omp2 gene, and 2 clones as part of the Omp3 gene, and 2 clones as part of the MOMP gene, indicating that COMC proteins had been successfully cloned. Furthermore, 32 clones were obtained, containing DNA sequences not found in the GenEmbl database. These sequences could, however, be clustered in two contigs of 6 and 4 clones, and three clones were identical. In addition 19 clones were found with no overlap to the contigs (Figure 7). To obtain more sequence data for the genes, *C. pneumoniae* DNA was totally digested with BamHI restriction enzyme, and the fragments were cloned into the vector pBluescript. The ligated DNA was electrotransformed into *E. coli* XL1-Blue and selected on plates containing Ampicillin. The recombinant bacterial colonies were transferred to a nitrocellulose membrane, and colony hybridisation was performed using the inserts of pEX 1-1 clone as a probe. A clone containing a single BamHI fragment of 4.5 kb was found, and the hybridisation to the probe was confirmed by Southern blotting. The insert of the clone was sequenced bi-directionally using synthetic primers for approx. each 300 bp. The sequence of the BamHI fragment made it possible to join the two contigs of pEX clones. Totally, together with the pEX clones it was possible to assemble 6.5 kb DNA sequence, encoding two new COMC proteins. (Figure 6)

Additional sequences were obtained by PCR performed on purified *C. pneumoniae* DNA with primers both from the known Omp genes and from other known genes. The obtained PCR

products were sequenced, The sequence organisation is shown in Fig. 7. Additional 8 Omp genes were detected. The alignment of the deduced amino acid sequences are shown in Fig. 8 A and B.

5 Analysis of DNA sequence

The DNA sequence encoding the Omp4-15 proteins with a size of 89.6-100.3 kDa (and for Omp13: 56.1 kDa). Omp4 and Omp5 were transcribed in opposite directions. Downstream Omp4 a possible termination structure was located. The 3' end of the Omp5 gene was not cloned due to the presence of the BamHI restriction enzyme site positioned within the gene. The translated DNA sequence of Omp4 and Omp5 was compared by use of the gap programme in the GCG package (Wisconsin package, version 8.1-UNIX, August 1995, sequence analysis software package). The two genes had an amino acid identity of 41% (similarity 61%), and a possible cleavage site for signal peptidase 1 was present at amino acid 17 in Omp4 and amino acid 25 in Omp5. When the amino acid sequence encoded by two other pEX clones were compared to the sequence of Omp4 and Omp5 they also had amino acid homology to the genes. It is seen that the two clones have homology to the same area in the Omp4 and Omp5 proteins. Consequently, the pEX clones must have originated from two additional genes. Therefore these genes were named Omp6 and Omp7. Similar analyses were performed with the other genes. In contrast to what was seen for Omp4 and 5 none of the other putative omp proteins had a cleavage site for signal peptides.

EXAMPLE 2

Polyclonal monospecific antibodies against pEX fusion proteins and full length recombination + Omp4

To investigate the topology of the Omp4-7 proteins, representative pEX clones, were selected from each gene. The fusion proteins of β -galactosidase/omp were induced, and the

proteins were partially purified as inclusion bodies. Balb/c mice were immunized three times intramuscular with the antigens at an interval of one week, and after six weeks the serum was obtained from the mice. HeLa cells were infected with the *C. pneumoniae*. 72 hours after the infection the mono-layers were fixed with 3.7% formaldehyde. This treatment makes the outer membrane of the Chlamydia impermeable for antibodies due to the extensive cross-linking of the outer membrane proteins by the formaldehyde. The HeLa cells were permeabilized with 0.2% Triton X100, the monolayers were washed in PBS, then incubated with 20% (v/v) FCS to inactivate free radicals of the formaldehyde. The mice sera were diluted 1:100 PBS with 20% (v/v) FCS and incubated with the monolayers for half an hour. The monolayers were washed in PBS and secondary FITCH conjugated rabbit anti mouse serum was added for half an hour, and the monolayers were washed and mounted. Several of the antibodies reacted strongly with the EBs in the inclusions (Figure 9). In spite of the formaldehyde fixation it could not be excluded that the surface of the EB was changed by the treatments, so that the antibodies could get access to the Omp4-7. Therefore, the reaction was confirmed by immuno-electron microscopy with the antibody raised against clone pEX3-36. Purified EB of *C. pneumoniae* were absorbed to carbon coated nickel grids. After the absorption the grids were washed with PBS and blocked in 0.5% Ovalbumin dissolved in PBS. The antibodies were diluted 1:100 in the same buffer and incubated for 30 minutes. The grids were washed in PBS. Rabbit anti mouse Ig conjugated with 10nm colloidal gold diluted in PBS containing 1% gelatin was added to the grids for half an hour. The grids were washed in 3 x PBS with 1% gelatin and 3 times in PBS, the grids were contraststained with 0.7% phospho tungstic acid. The grids were analysed in a Jeol 1010 electron microscope at 40 kV. It was seen that the gold particles were covering the surface of the purified EB. Because the *C. pneumoniae* EBs were not exposed to any detergent or fixation under either the purification or the reaction with antibodies, these

results show that the cloned proteins have surface exposed epitopes.

Polyclonal monospecific antibodies against Omp4

The Omp4 gene was amplified by PCR with primers that
5 contained LIC-sites, and the PCR product was cloned into the
pET-30 LIC vector (Novagen). The histidine tagged fusion
protein was expressed by induction of the synthesis by IPTG
and purified over a nickel column. The purified Omp4 protein
was used for immunization of a rabbit (six times, 8 μ g each
10 time).

Use of rabbit polyclonal antibodies to recombinant Omp4 for detection of *Chlamydia pneumoniae* in paraffin embedded sections

The lungs of *C. pneumoniae* infected mice were obtained three
15 days after intranasal infection. The tissue samples were
fixed in 4% formaldehyde, paraffin embedded, sectioned and
deparaffinized prior to staining. The sections were incubated
with the rabbit serum diluted 1:200 in TBS (150 mM NaCl,
20mM Tris pH 7.5) for 30 min at room temperature. After wash
20 two times in TBS the sections were incubated with the
secondary antibody (biotinylated goat anti-rabbit antibodies)
diluted 1:300 in TBS, followed by two times wash in TBS. The
sections were stained with streptavidin-biotin complex
(streptABComplex/AP, Dako) for 30 min washed and developed
25 under microscopic inspection with chromagen + new fuchsin
(Vector laboratories). The sections were counter stained with
Hematoxylin and analyzed ny microscopy.

Immuno blotting analysis with hyperimmune monospecific rabbit anti-serum

30 The insert of pEX1-1 clone was amplified by PCR using primers
containing LIC sites. The PCR product could therefore be
inserted in the pET-32 LIC vector (Novagen, UK cat No. 69076-

1). Thereby the insert sequence of the pEX1-1 clone was expressed in the new vector as a fusion protein, the part of the fusion protein encoded by the pET-32 LIC vector had 6 histidine residues in a row. The expression of the fusion protein was induced in this vector, and the fusion protein could be purified under denaturing condition on a Ni²⁺ column due to the high affinity of the histidine residues to divalent cations. The purified protein was used for immunization of a New Zealand white rabbit. After 6 times intramuscular and 2 times intravenous immunization the serum was obtained from the rabbit. Purified *C. pneumoniae* EB was dissolved in SDS-sample buffer. Half of the sample was heated to 100°C in the sample buffer, whereas the other half of the sample was not heated. The samples were separated by SDS-PAGE, and the proteins were transferred to nitrocellulose, the serum was reacted with the strips. With the samples heated to 100°C the serum recognized a high molecular weight band of approximately 98 kDa. This is in agreement with the predicted size of Omp5, of which the pEX1-1 clone is a part, however, when the antibody was reacted to the strip with unheated EB, the pattern was different. Now a band was seen with a size of 75 kDa, in addition weaker bands were observed above the band (Figure 10). These data demonstrate that Omp5 needs boiling in SDS-sample buffer to be fully denatured and migrate with a size as predicted from the gene product. When the samples were not boiled, the protein was not fully denatured and less SDS binds to the protein and it has a more globular structure that will migrate faster in the acrylamide gel. The band pattern looked identical to what was obtained with a monoclonal antibody (MAb 26.1) (lane 6), we earlier have described (Christiansen et al., 1994), reacting with the surface of *C. pneumoniae* EB, but the antibody do not react with the fully SDS denatured *C. pneumoniae* EB in immunoblotting.

Experimental infection of C57 black mice

Due to the realization of the altered migration of the Omp4-7 proteins without boiling, we chose to analyse antibodies against *C. pneumoniae* EBs after an experimental infection of mice. To obtain antibodies from an infection caused by *C. pneumoniae*, C57 black mice were inoculated intranasally with 10^7 CFI of *C. pneumoniae* under a light ether anaesthesia. After 14 days of infection the serum samples were obtained and the lungs were analysed for pathological changes. In two of the mice a severe pneumonia was observed in the lung sections, and in the third mouse only minor changes were observed. The serum from the mice was diluted 1:100 and reacted with purified EBs dissolved in sample buffer with and without boiling. In the preparations that had been heated to 100°C the sera from two of the mice reacted strongly with bands of 60/62 kDa and weaker bands of 55 kDa, but no reaction was observed with proteins of the size of Omp4-7 (Figure 11). However, when the sera were reacted with the preparation that had not been heated they all had a strong reaction with a broad band of an approximate size of 75 kDa. This is in agreement with the size of the Omp4-7 proteins in the unheated preparation. Therefore, it could be concluded that the epitopes of the Omp4-7 proteins recognized by the antibodies after a *C. pneumoniae* infection were discontinuous epitopes because the full denaturation of the antigen completely destroyed the epitopes. The 75 kDa protein observed in unheated samples is not Omp2 (Shown in immunoblotting with an Omp2 specific antibody)

EXAMPLE 3

Comparison of Omp4-7 of *C. pneumoniae* with putative outer membrane proteins (POMP) of *C. psittaci*

Longbottom et al. (1996) have published partial sequence from 98 to 90 kDa proteins from *C. psittaci*. They have entered the full sequence of 5 genes in this family in the EMBL database.

They have named the genes "putative outer membrane proteins" (POMP) since their precise location was not determined. The family is composed of two genes that are completely identical, and two genes with high homology to these genes.

5 They calculated a molecular size of 90 and 91 kDa. The 5th encode a protein of 98 kDa. The sequence of the Omp4-7 proteins of *C. pneumoniae* were compared to the sequences of the *C. Psittaci* POMP proteins with the programme pileup in the GCG package. The amino acid homologies were in the range
10 of 51-63%. It is seen that the *C. pneumoniae* Omp4-5 proteins are most related to the 98 kDa POMP protein of *C. psittaci*. Interestingly, the 98 kDa *C. psittaci* POMP protein is more related to the *C. pneumoniae* genes than to the other *C. psittaci* genes. The repeated sequences of GGAI were conserved
15 in the 98 kDa POMP protein, but only three GGAI repeats were present in the 90 and 91 kDa *C. psittaci* POMP proteins. For *C. psittaci* it has been shown that antibodies to these proteins seem to be protective for the infection.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT

- (A) NAME: Svend Birkelund
 (B) STREET: Dept. of Medical Microbiology and Immunology,
 University of Århus
 (C) CITY: Århus C
 (D) STATE OR PROVINCE:
 (E) COUNTRY: Denmark
 (F) POSTAL CODE: 8000

(ii) TITLE OF THE INVENTION: Chlamydia pneumoniae anti
 gens

(iii) NUMBER OF SEQUENCES: 30

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 205...2987
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGTCGAA	GAGAGCACTA	ACCAGGAAAA	TTGCGATTTC	ATAAACCCAC	TTTATTATTA	60
AATTCTTACT	TGCGTCATAT	AAAATAGAAA	ACTCAGAGAG	TCAAGATAAA	AATTCTTGAC	120
AGCTGTTTTG	TCATCTTTAA	CTTGATTTAC	TTATTTTGTT	TCTATATTGA	TGCGAATAGT	180
TCTCTAAAAA	ACAAAAGCAT	TACC ATG AAG ACT	TCG ATT CCT	TGG GTT TTA		231
		Met Lys Thr Ser Ile	Pro Trp Val Leu			
		1	5			
GTT TCC TCC	GTG TTA GCT	TTC TCA TGT	CAC CTA CAG	TCA CTA GCT	AAC	279
Val Ser Ser	Val Leu Ala	Phe Ser Cys	His Leu Gln	Ser Leu Ala	Asn	
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GAG GAA CTT TTA TCA CCT GAT GAT AGC TTT AAT GGA AAT ATC GAT TCA	327
Glu Glu Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly Asn Ile Asp Ser	
30 35 40	
GGA ACG TTT ACT CCA AAA ACT TCA GCC ACA ACA TAT TCT CTA ACA GGA	375
Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr Ser Leu Thr Gly	
45 50 55	
GAT GTC TTC TTT TAC GAG CCT GGA AAA GGC ACT CCC TTA TCT GAC AGT	423
Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro Leu Ser Asp Ser	
60 65 70	
TGT TTT AAG CAA ACC ACG GAC AAT CTT ACC TTC TTG GGG AAC GGT CAT	471
Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu Gly Asn Gly His	
75 80 85	
AGC TTA ACG TTT GGC TTT ATA GAT GCT GGC ACT CAT GCA GGT GCT GCT	519
Ser Leu Thr Phe Gly Phe Ile Asp Ala Gly Thr His Ala Gly Ala Ala	
90 95 100 105	
GCA TCT ACA ACA GCA AAT AAG AAT CTT ACC TTC TCA GGG TTT TCC TTA	567
Ala Ser Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser Gly Phe Ser Leu	
110 115 120	
CTG AGT TTT GAT TCC TCT CCT AGC ACA ACG GTT ACT ACA GGT CAG GGA	615
Leu Ser Phe Asp Ser Ser Pro Ser Thr Thr Val Thr Thr Gly Gln Gly	
125 130 135	
ACG CTT TCC TCA GCA GGA GGC GTA AAT TTA GAA AAT ATT CGT AAA CTT	663
Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn Ile Arg Lys Leu	
140 145 150	
GTA GTT GCT GGG AAT TTT TCT ACT GCA GAT GGT GGA GCT ATC AAA GGA	711
Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly Ala Ile Lys Gly	
155 160 165	
GCG TCT TTC CTT TTA ACT GGC ACT TCT GGA GAT GCT CTT TTT AGT AAC	759
Ala Ser Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala Leu Phe Ser Asn	
170 175 180 185	
AAC TCT TCA TCA ACA AAG GGA GGA GCA ATT GCT ACT ACA GCA GGC GCT	807
Asn Ser Ser Ser Thr Lys Gly Gly Ala Ile Ala Thr Thr Ala Gly Ala	
190 195 200	
CGC ATA GCA AAT AAC ACA GGT TAT GTT AGA TTC CTA TCT AAC ATA GCG	855
Arg Ile Ala Asn Asn Thr Gly Tyr Val Arg Phe Leu Ser Asn Ile Ala	
205 210 215	
TCT ACG TCA GGA GGC GCT ATC GAT GAT GAA GGC ACG TCG ATA CTA TCG	903
Ser Thr Ser Gly Gly Ala Ile Asp Asp Glu Gly Thr Ser Ile Leu Ser	
220 225 230	
AAC AAC AAA TTT CTA TAT TTT GAA GGG AAT GCA GCG AAA ACT ACT GGC	951
Asn Asn Lys Phe Leu Tyr Phe Glu Gly Asn Ala Ala Lys Thr Thr Gly	
235 240 245	
GGT GCG ATC TGC AAC ACC AAG GCG AGT GGA TCT CCT GAA CTG ATA ATC	999

Gly 250	Ala	Ile	Cys	Asn	Thr 255	Lys	Ala	Ser	Gly 260	Ser	Pro	Glu	Leu	Ile	Ile 265	
TCT	AAC	AAT	AAG	ACT	CTG	ATC	TTT	GCT	TCA	AAC	GTA	GCA	GAA	ACA	AGC	1047
Ser	Asn	Asn	Lys	Thr 270	Leu	Ile	Phe	Ala	Ser 275	Asn	Val	Ala	Glu	Thr	Ser 280	
GGT	GGC	GCC	ATC	CAT	GCT	AAA	AAG	CTA	GCC	CTT	TCC	TCT	GGA	GGC	TTT	1095
Gly	Gly	Ala	Ile 285	His	Ala	Lys	Lys	Leu 290	Ala	Leu	Ser	Ser	Gly	Gly	Phe 295	
ACA	GAG	TTT	CTA	CGA	AAT	AAT	GTC	TCA	TCA	GCA	ACT	CCT	AAG	GGG	GGT	1143
Thr	Glu	Phe	Leu	Arg	Asn	Asn	Val 305	Ser	Ser	Ala	Thr 310	Pro	Lys	Gly	Gly	
GCT	ATC	AGC	ATC	GAT	GCC	TCA	GGA	GAG	CTC	AGT	CTT	TCT	GCA	GAG	ACA	1191
Ala	Ile	Ser	Ile	Asp	Ala	Ser	Gly 320	Glu	Leu	Ser	Leu 325	Ser	Ala	Glu	Thr	
GGA	AAC	ATT	ACC	TTT	GTA	AGA	AAT	ACC	CTT	ACA	ACA	ACC	GGA	AGT	ACC	1239
Gly	Asn	Ile	Thr	Phe	Val	Arg	Asn	Thr	Leu	Thr	Thr	Thr	Gly	Ser	Thr 345	
330					335				340							
GAT	ACT	CCT	AAA	CGT	AAT	GCG	ATC	AAC	ATA	GGA	AGT	AAC	GGG	AAA	TTC	1287
Asp	Thr	Pro	Lys	Arg	Asn	Ala	Ile	Asn	Ile	Gly	Ser	Asn	Gly	Lys	Phe 360	
				350				355								
ACG	GAA	TTA	CGG	GCT	GCT	AAA	AAT	CAT	ACA	ATT	TTC	TTC	TAT	GAT	CCC	1335
Thr	Glu	Leu	Arg	Ala	Ala	Lys	Asn	His	Thr	Ile	Phe	Phe	Tyr	Asp	Pro	
			365				370						375			
ATC	ACT	TCA	GAA	GGA	ACC	TCA	TCA	GAC	GTA	TTG	AAG	ATA	AAT	AAC	GGC	1383
Ile	Thr	Ser	Glu	Gly	Thr	Ser	Ser	Asp	Val	Leu	Lys	Ile	Asn	Asn	Gly	
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TCT	GCG	GGA	GCT	CTC	AAT	CCA	TAT	CAA	GGA	ACG	ATT	CTA	TTT	TCT	GGA	1431
Ser	Ala	Gly	Ala	Leu	Asn	Pro	Tyr	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Gly	
	395				400						405					
GAA	ACC	CTA	ACA	GCA	GAT	GAA	CTT	AAA	GTT	GCT	GAC	AAT	TTA	AAA	TCT	1479
Glu	Thr	Leu	Thr	Ala	Asp	Glu	Leu	Lys	Val	Ala	Asp	Asn	Leu	Lys	Ser	
410					415				420					425		
TCA	TTC	ACG	CAG	CCA	GTC	TCC	CTA	TCC	GGA	GGA	AAG	TTA	TTG	CTA	CAA	1527
Ser	Phe	Thr	Gln	Pro	Val	Ser	Leu	Ser	Gly	Gly	Lys	Leu	Leu	Leu	Gln	
				430					435					440		
AAG	GGA	GTC	ACT	TTA	GAG	AGC	ACG	AGC	TTC	TCT	CAA	GAG	GCC	GGT	TCT	1575
Lys	Gly	Val	Thr	Leu	Glu	Ser	Thr	Ser	Phe	Ser	Gln	Glu	Ala	Gly	Ser	
			445				450					455				
CTC	CTC	GGC	ATG	GAT	TCA	GGA	ACG	ACA	TTA	TCA	ACT	ACA	GCT	GGG	AGT	1623
Leu	Leu	Gly	Met	Asp	Ser	Gly	Thr	Thr	Leu	Ser	Thr	Thr	Ala	Gly	Ser	
		460				465					470					
ATT	ACA	ATC	ACG	AAC	CTA	GGA	ATC	AAT	GTT	GAC	TCC	TTA	GGT	CTT	AAG	1671
Ile	Thr	Ile	Thr	Asn	Leu	Gly	Ile	Asn	Val	Asp	Ser	Leu	Gly	Leu	Lys	

475	480	485	
CAG CCC GTC AGC CTA ACA GCA AAA GGT GCT TCA AAT AAA GTG ATC GTA Gln Pro Val Ser Leu Thr Ala Lys Gly Ala Ser Asn Lys Val Ile Val 490 495 500 505			1719
TCT GGG AAG CTC AAC CTG ATT GAT ATT GAA GGG AAC ATT TAT GAA AGT Ser Gly Lys Leu Asn Leu Ile Asp Ile Glu Gly Asn Ile Tyr Glu Ser 510 515 520			1767
CAT ATG TTC AGC CAT GAC CAG CTC TTC TCT CTA TTA AAA ATC ACG GTT His Met Phe Ser His Asp Gln Leu Phe Ser Leu Leu Lys Ile Thr Val 525 530 535			1815
GAT GCT GAT GTT GAT ACT AAC GTT GAC ATC AGC AGC CTT ATC CCT GTT Asp Ala Asp Val Asp Thr Asn Val Asp Ile Ser Ser Leu Ile Pro Val 540 545 550			1863
CCT GCT GAG GAT CCT AAT TCA GAA TAC GGA TTC CAA GGA CAA TGG AAT Pro Ala Glu Asp Pro Asn Ser Glu Tyr Gly Phe Gln Gly Gln Trp Asn 555 560 565			1911
GTT AAT TGG ACT ACG GAT ACA GCT ACA AAT ACA AAA GAG GCC ACG GCA Val Asn Trp Thr Thr Asp Thr Ala Thr Asn Thr Lys Glu Ala Thr Ala 570 575 580 585			1959
ACT TGG ACC AAA ACA GGA TTT GTT CCC AGC CCC GAA AGA AAA TCT GCG Thr Trp Thr Lys Thr Gly Phe Val Pro Ser Pro Glu Arg Lys Ser Ala 590 595 600			2007
TTA GTA TGC AAT ACC CTA TGG GGA GTC TTT ACT GAC ATT CGC TCT CTG Leu Val Cys Asn Thr Leu Trp Gly Val Phe Thr Asp Ile Arg Ser Leu 605 610 615			2055
CAA CAG CTT GTA GAG ATC GGC GCA ACT GGT ATG GAA CAC AAA CAA GGT Gln Gln Leu Val Glu Ile Gly Ala Thr Gly Met Glu His Lys Gln Gly 620 625 630			2103
TTC TGG GTT TCC TCC ATG ACG AAC TTC CTG CAT AAG ACT GGA GAT GAA Phe Trp Val Ser Ser Met Thr Asn Phe Leu His Lys Thr Gly Asp Glu 635 640 645			2151
AAT CGC AAA GGC TTC CGT CAT ACC TCT GGA GGC TAC GTC ATC GGT GGA Asn Arg Lys Gly Phe Arg His Thr Ser Gly Gly Tyr Val Ile Gly Gly 650 655 660 665			2199
AGT GCT CAC ACT CCT AAA GAC GAC CTA TTT ACC TTT GCG TTC TGC CAT Ser Ala His Thr Pro Lys Asp Asp Leu Phe Thr Phe Ala Phe Cys His 670 675 680			2247
CTC TTT GCT AGA GAC AAA GAT TGT TTT ATC GCT CAC AAC AAC TCT AGA Leu Phe Ala Arg Asp Lys Asp Cys Phe Ile Ala His Asn Asn Ser Arg 685 690 695			2295
ACC TAC GGT GGA ACT TTA TTC TTC AAG CAC TCT CAT ACC CTA CAA CCC Thr Tyr Gly Gly Thr Leu Phe Phe Lys His Ser His Thr Leu Gln Pro 700 705 710			2343

CAA AAC TAT TTG AGA TTA GGA AGA GCA AAG TTT TCT GAA TCA GCT ATA Gln Asn Tyr Leu Arg Leu Gly Arg Ala Lys Phe Ser Glu Ser Ala Ile 715 720 725	2391
GAA AAA TTC CCT AGG GAA ATT CCC CTA GCC TTG GAT GTC CAA GTT TCG Glu Lys Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp Val Gln Val Ser 730 735 740 745	2439
TTC AGC CAT TCA GAC AAC CGT ATG GAA ACG CAC TAT ACC TCA TTG CCA Phe Ser His Ser Asp Asn Arg Met Glu Thr His Tyr Thr Ser Leu Pro 750 755 760	2487
GAA TCC GAA GGT TCT TGG AGC AAC GAG TGT ATA GCT GGT GGT ATC GGC Glu Ser Glu Gly Ser Trp Ser Asn Glu Cys Ile Ala Gly Gly Ile Gly 765 770 775	2535
CTA GAC CTT CCT TTT GTT CTT TCC AAC CCA CAT CCT CTT TTC AAG ACC Leu Asp Leu Pro Phe Val Leu Ser Asn Pro His Pro Leu Phe Lys Thr 780 785 790	2583
TTC ATT CCA CAG ATG AAA GTC GAA ATG GTT TAT GTA TCA CAA AAT AGC Phe Ile Pro Gln Met Lys Val Glu Met Val Tyr Val Ser Gln Asn Ser 795 800 805	2631
TTC TTC GAA AGC TCT AGT GAT GGC CGT GGT TTT AGT ATT GGA AGG CTG Phe Phe Glu Ser Ser Ser Asp Gly Arg Gly Phe Ser Ile Gly Arg Leu 810 815 820 825	2679
CTT AAC CTC TCG ATT CCT GTG GGT GCG AAA TTC GTG CAG GGG GAT ATC Leu Asn Leu Ser Ile Pro Val Gly Ala Lys Phe Val Gln Gly Asp Ile 830 835 840	2727
GGA GAT TCC TAC ACC TAT GAT CTC TCA GGA TTC TTT GTT TCC GAT GTC Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe Val Ser Asp Val 845 850 855	2775
TAT CGT AAC AAT CCC CAA TCT ACA GCG ACT CTT GTG ATG AGC CCA GAC Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val Met Ser Pro Asp 860 865 870	2823
TCT TGG AAA ATT CGC GGT GGC AAT CTT TCA AGA CAG GCA TTT TTA CTG Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln Ala Phe Leu Leu 875 880 885	2871
AGG GGT AGC AAC AAC TAC GTC TAC AAC TCC AAT TGT GAG CTC TTC GGA Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys Glu Leu Phe Gly 890 895 900 905	2919
CAT TAC GCT ATG GAA CTC CGT GGA TCT TCA AGG AAC TAC AAT GTA GAT His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn Tyr Asn Val Asp 910 915 920	2967
GTT GGT ACC AAA CTC CGA TT CTAGATTGCT AAAACTCCCT AGTTCTTCTA GGGAG Val Gly Thr Lys Leu Arg Phe 925	3022
TTTTCTCATA CTTTtaggga AATATTGCT ATAGGGAATG CTTTCCTTGC AAAGTGTAAA	3082

AAATAACATT TGTCCCTCTT CAAAAAAGAT TTCTTTTAAT AATTTCTAGT TATAATTTTA 3142
 TTTTAAAAAC AGTTAAATAA TTAATAGACA ATAATCTATT CTTATTGACT TCTTTTTT 3200

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Thr	Ser	Ile	Pro	Trp	Val	Leu	Val	Ser	Ser	Val	Leu	Ala	Phe
1				5					10					15	
Ser	Cys	His	Leu	Gln	Ser	Leu	Ala	Asn	Glu	Glu	Leu	Leu	Ser	Pro	Asp
			20					25				30			
Asp	Ser	Phe	Asn	Gly	Asn	Ile	Asp	Ser	Gly	Thr	Phe	Thr	Pro	Lys	Thr
		35					40					45			
Ser	Ala	Thr	Thr	Tyr	Ser	Leu	Thr	Gly	Asp	Val	Phe	Phe	Tyr	Glu	Pro
	50					55				60					
Gly	Lys	Gly	Thr	Pro	Leu	Ser	Asp	Ser	Cys	Phe	Lys	Gln	Thr	Thr	Asp
65					70				75					80	
Asn	Leu	Thr	Phe	Leu	Gly	Asn	Gly	His	Ser	Leu	Thr	Phe	Gly	Phe	Ile
			85					90					95		
Asp	Ala	Gly	Thr	His	Ala	Gly	Ala	Ala	Ala	Ser	Thr	Thr	Ala	Asn	Lys
		100					105						110		
Asn	Leu	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Leu	Ser	Phe	Asp	Ser	Ser	Pro
	115						120					125			
Ser	Thr	Thr	Val	Thr	Thr	Gly	Gln	Gly	Thr	Leu	Ser	Ser	Ala	Gly	Gly
	130					135					140				
Val	Asn	Leu	Glu	Asn	Ile	Arg	Lys	Leu	Val	Val	Ala	Gly	Asn	Phe	Ser
145					150				155					160	
Thr	Ala	Asp	Gly	Gly	Ala	Ile	Lys	Gly	Ala	Ser	Phe	Leu	Leu	Thr	Gly
			165					170					175		
Thr	Ser	Gly	Asp	Ala	Leu	Phe	Ser	Asn	Asn	Ser	Ser	Ser	Thr	Lys	Gly
		180					185						190		
Gly	Ala	Ile	Ala	Thr	Thr	Ala	Gly	Ala	Arg	Ile	Ala	Asn	Asn	Thr	Gly
	195					200					205				
Tyr	Val	Arg	Phe	Leu	Ser	Asn	Ile	Ala	Ser	Thr	Ser	Gly	Gly	Ala	Ile
	210					215					220				
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225					230				235					240	
Glu	Gly	Asn	Ala	Ala	Lys	Thr	Thr	Gly	Gly	Ala	Ile	Cys	Asn	Thr	Lys
			245					250					255		
Ala	Ser	Gly	Ser	Pro	Glu	Leu	Ile	Ile	Ser	Asn	Asn	Lys	Thr	Leu	Ile
		260					265						270		
Phe	Ala	Ser	Asn	Val	Ala	Glu	Thr	Ser	Gly	Gly	Ala	Ile	His	Ala	Lys
	275						280					285			
Lys	Leu	Ala	Leu	Ser	Ser	Gly	Gly	Phe	Thr	Glu	Phe	Leu	Arg	Asn	Asn
	290					295				300					
Val	Ser	Ser	Ala	Thr	Pro	Lys	Gly	Gly	Ala	Ile	Ser	Ile	Asp	Ala	Ser

305		310		315		320									
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		325							330					335	
Asn	Thr	Leu	Thr	Thr	Thr	Gly	Ser	Thr	Asp	Thr	Pro	Lys	Arg	Asn	Ala
		340							345				350		
Ile	Asn	Ile	Gly	Ser	Asn	Gly	Lys	Phe	Thr	Glu	Leu	Arg	Ala	Ala	Lys
		355					360					365			
Asn	His	Thr	Ile	Phe	Phe	Tyr	Asp	Pro	Ile	Thr	Ser	Glu	Gly	Thr	Ser
		370					375					380			
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385					390					395				400	
Tyr	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Gly	Glu	Thr	Leu	Thr	Ala	Asp	Glu
			405						410					415	
Leu	Lys	Val	Ala	Asp	Asn	Leu	Lys	Ser	Ser	Phe	Thr	Gln	Pro	Val	Ser
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Leu	Ser	Gly	Gly	Lys	Leu	Leu	Leu	Gln	Lys	Gly	Val	Thr	Leu	Glu	Ser
		435					440					445			
Thr	Ser	Phe	Ser	Gln	Glu	Ala	Gly	Ser	Leu	Leu	Gly	Met	Asp	Ser	Gly
		450				455					460				
Thr	Thr	Leu	Ser	Thr	Thr	Ala	Gly	Ser	Ile	Thr	Ile	Thr	Asn	Leu	Gly
465					470					475				480	
Ile	Asn	Val	Asp	Ser	Leu	Gly	Leu	Lys	Gln	Pro	Val	Ser	Leu	Thr	Ala
			485						490					495	
Lys	Gly	Ala	Ser	Asn	Lys	Val	Ile	Val	Ser	Gly	Lys	Leu	Asn	Leu	Ile
			500					505					510		
Asp	Ile	Glu	Gly	Asn	Ile	Tyr	Glu	Ser	His	Met	Phe	Ser	His	Asp	Gln
		515					520					525			
Leu	Phe	Ser	Leu	Leu	Lys	Ile	Thr	Val	Asp	Ala	Asp	Val	Asp	Thr	Asn
	530				535						540				
Val	Asp	Ile	Ser	Ser	Leu	Ile	Pro	Val	Pro	Ala	Glu	Asp	Pro	Asn	Ser
545					550					555				560	
Glu	Tyr	Gly	Phe	Gln	Gly	Gln	Trp	Asn	Val	Asn	Trp	Thr	Thr	Asp	Thr
			565						570					575	
Ala	Thr	Asn	Thr	Lys	Glu	Ala	Thr	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Phe
		580						585					590		
Val	Pro	Ser	Pro	Glu	Arg	Lys	Ser	Ala	Leu	Val	Cys	Asn	Thr	Leu	Trp
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Gly	Val	Phe	Thr	Asp	Ile	Arg	Ser	Leu	Gln	Gln	Leu	Val	Glu	Ile	Gly
	610					615					620				
Ala	Thr	Gly	Met	Glu	His	Lys	Gln	Gly	Phe	Trp	Val	Ser	Ser	Met	Thr
625					630					635				640	
Asn	Phe	Leu	His	Lys	Thr	Gly	Asp	Glu	Asn	Arg	Lys	Gly	Phe	Arg	His
			645						650					655	
Thr	Ser	Gly	Gly	Tyr	Val	Ile	Gly	Gly	Ser	Ala	His	Thr	Pro	Lys	Asp
		660					665						670		
Asp	Leu	Phe	Thr	Phe	Ala	Phe	Cys	His	Leu	Phe	Ala	Arg	Asp	Lys	Asp
		675					680					685			
Cys	Phe	Ile	Ala	His	Asn	Asn	Ser	Arg	Thr	Tyr	Gly	Gly	Thr	Leu	Phe
	690					695					700				
Phe	Lys	His	Ser	His	Thr	Leu	Gln	Pro	Gln	Asn	Tyr	Leu	Arg	Leu	Gly
705					710					715				720	
Arg	Ala	Lys	Phe	Ser	Glu	Ser	Ala	Ile	Glu	Lys	Phe	Pro	Arg	Glu	Ile
			725						730					735	
Pro	Leu	Ala	Leu	Asp	Val	Gln	Val	Ser	Phe	Ser	His	Ser	Asp	Asn	Arg
			740					745					750		
Met	Glu	Thr	His	Tyr	Thr	Ser	Leu	Pro	Glu	Ser	Glu	Gly	Ser	Trp	Ser
		755					760					765			

Asn	Glu	Cys	Ile	Ala	Gly	Gly	Ile	Gly	Leu	Asp	Leu	Pro	Phe	Val	Leu
770						775					780				
Ser	Asn	Pro	His	Pro	Leu	Phe	Lys	Thr	Phe	Ile	Pro	Gln	Met	Lys	Val
785					790					795					800
Glu	Met	Val	Tyr	Val	Ser	Gln	Asn	Ser	Phe	Phe	Glu	Ser	Ser	Ser	Asp
				805					810					815	
Gly	Arg	Gly	Phe	Ser	Ile	Gly	Arg	Leu	Leu	Asn	Leu	Ser	Ile	Pro	Val
			820				825						830		
Gly	Ala	Lys	Phe	Val	Gln	Gly	Asp	Ile	Gly	Asp	Ser	Tyr	Thr	Tyr	Asp
	835						840					845			
Leu	Ser	Gly	Phe	Phe	Val	Ser	Asp	Val	Tyr	Arg	Asn	Asn	Pro	Gln	Ser
850						855					860				
Thr	Ala	Thr	Leu	Val	Met	Ser	Pro	Asp	Ser	Trp	Lys	Ile	Arg	Gly	Gly
865					870					875					880
Asn	Leu	Ser	Arg	Gln	Ala	Phe	Leu	Leu	Arg	Gly	Ser	Asn	Asn	Tyr	Val
				885					890					895	
Tyr	Asn	Ser	Asn	Cys	Glu	Leu	Phe	Gly	His	Tyr	Ala	Met	Glu	Leu	Arg
			900					905					910		
Gly	Ser	Ser	Arg	Asn	Tyr	Asn	Val	Asp	Val	Gly	Thr	Lys	Leu	Arg	Phe
	915						920							925	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2815 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATCGC	AATTTTCCTG	GTTAGTGCTC	TCTTCGACAT	TGGCATGTTT	TACTAGTTGT	60
TCCACTGTTT	TTGCTGCAAC	TGCTGAAAAT	ATAGGCCCTT	CTGATAGCTT	TGACGGAAGT	120
ACTAACACAG	GCACCTATAC	TCCTAAAAAT	ACGACTACTG	GAATAGACTA	TACTCTGACA	180
GGAGATATAA	CTCTGCAAAA	CCTTGGGGAT	TCGGCAGCTT	TAACGAAGGG	TTGTTTTTCT	240
GACACTACGG	AATCTTTAAG	CTTTGCCGGT	AAGGGGTACT	CACTTTCTTT	TTTAAATATT	300
AAGTCTAGTG	CTGAAGGCGC	AGCACTTTCT	GTTACAACCTG	ATAAAAATCT	GTCGCTAACA	360
GGATTTTCGA	GTCTTACTTT	CTTAGCGGCC	CCATCATCGG	TAATCACAAC	CCCCTCAGGA	420
AAAGGTGCAG	TTAAATGTGG	AGGGGATCTT	ACATTTGATA	ACAATGGAAC	TATTTTATTT	480
AAACAAGATT	ACTGTGAGGA	AAATGGCGGA	GCCATTTCTA	CCAAGAATCT	TTCTTTGAAA	540
AACAGCACGG	GATCGATTTT	TTTTGAAGGG	AATAAATCGA	GCGCAACAGG	GAAAAAAGGT	600
GGGGCTATTT	GTGCTACTGG	TACTGTAGAT	ATTACAAATA	ATACGGCTCC	TACCCTCTTC	660
TCGAACAATA	TTGCTGAAGC	TGCAGGTGGA	GCTATAAATA	GCACAGGAAA	CTGTACAATT	720
ACAGGGAATA	CGTCTCTTGT	ATTTTCTGAA	AATAGTGTGA	CAGCGACCGC	AGGAAATGGA	780
GGAGCTCTTT	CTGGAGATGC	CGATGTTACC	ATATCTGGGA	ATCAGAGTGT	AACTTTCTCA	840
GGAAACCAAG	CTGTAGCTAA	TGGCGGAGCC	ATTTATGCTA	AGAAGCTTAC	ACTGGCTTCC	900
GGGGGGGGGG	GGGGTATCTC	CTTTTCTAAG	AATATAGTCC	AAGGTACCAC	TGCAGGTAAT	960
GGTGGAGCCA	TTTCTATACT	GGCAGTATGA	GAGTGTAGTC	TTTCAGCAGA	AGCAGGGGAC	1020
ATTACCTTCA	ATGGGAATGC	CATTGTTGCA	ACTACACCAC	AAACTACAAA	AAGAAATTCT	1080
ATTGACATAG	GATCTACTGC	AAAGATCACG	AATTTACGTG	CAATATCTGG	GCATAGCATC	1140
TTTTTCTACG	ATCCGATTAC	TGCTAATACG	GCTGCGGATT	CTACAGATAC	TTTAAATCTC	1200
AATAAGGCTG	ATGCAGGTAA	TAGTACAGAT	TATAGTGGGT	CGATTGTTTT	TTCTGGTGAA	1260

AAGCTCTCTG	AAGATGAAGC	AAAAGTTGCA	GACAACCTCA	CTTCTACGCT	GAAGCAGCCT	1320
GTAAGTCTAA	CTGCAGGAAA	TTTAGTACTT	AAACGTGGTG	TCACTCTCGA	TACGAAAGGC	1380
TTTACTCAGA	CCGCGGGTTC	CTCTGTTATT	ATGGATGCGG	GCACAACGTT	AAAAGCAAGT	1440
ACAGAGGAGG	TCACTTTAAC	AGGTCTTTCC	ATTCTGTAG	ACTCTTTAGG	CGAGGGTAAG	1500
AAAGTTGTAA	TTGCTGCTTC	TGCAGCAAGT	AAAAATGTAG	CCCTTAGTGG	TCCGATTCTT	1560
CTTTTGGATA	ACCAAGGGAA	TGCTTATGAA	AATCACGACT	TAGGAAAAAC	TCAAGACTTT	1620
TCATTTGTGC	AGCTCTCTGC	TCTGGGTACT	GCAACAACCTA	CAGATGTTCC	AGCGGTTCTT	1680
ACAGTAGCAA	CTCCTACGCA	CTATGGGTAT	CAAGGTACTT	GGGGAATGAC	TTGGGTTGAT	1740
GATACCGCAA	GCACTCCAAA	GACTAAGACA	GCGACATTAG	CTTGGACCAA	TACAGGCTAC	1800
CTTCCGAATC	CTGAGCGTCA	AGGACCTTTA	GTTCCCTAATA	GCCTTTGGGG	ATCTTTTTC	1860
GACATCCAAG	CGATTCAAGG	TGTCATAGAG	AGAAGTGCTT	TGACTCTTTG	TTCAGATCGA	1920
GGCTTCTGGG	CTGCGGGAGT	CGCCAATTTT	TTAGATAAAG	ATAAGAAAGG	GGAAAAACGC	1980
AAATACCGTC	ATAAATCTGG	TGGATATGCT	ATCGGAGGTG	CAGCGCAAAC	TTGTTCTGAA	2040
AACTTAATTA	GCTTTGCCTT	TTGCCAACTC	TTTGGTAGCG	ATAAAGATTT	CTTAGTCGCT	2100
AAAAATCATA	CTGATACCTA	TGCAGGAGCC	TTCTATATCC	AACACATTAC	AGAATGTAGT	2160
GGGTTCATAG	GTTGTCTCTT	AGATAAACTT	CCTGGCTCTT	GGAGTCATAA	ACCCCTCGTT	2220
TTAGAAGGGC	AGCTCGCTTA	TAGCCACGTC	AGTAATGATC	TGAAGACAAA	GTATACTGCG	2280
TATCCTGAGG	TGAAAGGTTT	TTGGGGGAAT	AATGCTTTTA	ACATGATGTT	GGGAGCTTCT	2340
TCTCATTCTT	ATCCTGAATA	CCTGCATTGT	TTTGATACCT	ATGCTCCATA	CATCAAACCTG	2400
AATCTGACCT	ATATACGTCA	GGACAGCTTC	TCGGAGAAAAG	GTACAGAAGG	AAGATCTTTT	2460
GATGACAGCA	ACCTCTTCAA	TTTATCTTTG	CCTATAGGGG	TGAAGTTTGA	GAAGTTCTCT	2520
GATTGTAATG	ACTTTTCTTA	TGATCTGACT	TTATCCTATG	TTCTGATCT	TATCCGCAAT	2580
GATCCCAAAT	GCACTACAGC	ACTTGTAATC	AGCGGAGCCT	CTTGGGAAAC	TTATGCCAAT	2640
AACTTAGCAC	GACAGGCCTT	GCAAGTGCGT	GCAGGCAGTC	ACTACGCCTT	CTCTCCTATG	2700
TTTGAAGTGC	TCGGCCAGTT	TGTCTTTGAA	GTTCTGTGGT	CCTCACGGAT	TTATAATGTA	2760
GATCTTGGGG	GTAAGTTCCA	ATTCTAGGAG	CGTCTCTCAT	GTCTCAGAAA	TTCTG	2815

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Ser	Gln	Phe	Ser	Trp	Leu	Val	Leu	Ser	Ser	Thr	Leu	Ala	Cys
1				5					10					15	
Phe	Thr	Ser	Cys	Ser	Thr	Val	Phe	Ala	Ala	Thr	Ala	Glu	Asn	Ile	Gly
			20					25					30		
Pro	Ser	Asp	Ser	Phe	Asp	Gly	Ser	Thr	Asn	Thr	Gly	Thr	Tyr	Thr	Pro
		35					40					45			
Lys	Asn	Thr	Thr	Thr	Gly	Ile	Asp	Tyr	Thr	Leu	Thr	Gly	Asp	Ile	Thr
	50					55					60				
Leu	Gln	Asn	Leu	Gly	Asp	Ser	Ala	Ala	Leu	Thr	Lys	Gly	Cys	Phe	Ser
65					70				75					80	
Asp	Thr	Thr	Glu	Ser	Leu	Ser	Phe	Ala	Gly	Lys	Gly	Tyr	Ser	Leu	Ser
			85					90						95	
Phe	Leu	Asn	Ile	Lys	Ser	Ser	Ala	Glu	Gly	Ala	Ala	Leu	Ser	Val	Thr
		100					105						110		
Thr	Asp	Lys	Asn	Leu	Ser	Leu	Thr	Gly	Phe	Ser	Ser	Leu	Thr	Phe	Leu
	115					120						125			
Ala	Ala	Pro	Ser	Ser	Val	Ile	Thr	Thr	Pro	Ser	Gly	Lys	Gly	Ala	Val
	130					135					140				

Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe
 145 150 155 160
 Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn
 165 170 175
 Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys
 180 185 190
 Ser Ser Ala Thr Gly Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr
 195 200 205
 Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile
 210 215 220
 Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile
 225 230 235 240
 Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr
 245 250 255
 Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser
 260 265 270
 Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly
 275 280 285
 Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly
 290 295 300
 Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn
 305 310 315 320
 Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser Leu Ser Ala
 325 330 335
 Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val Ala Thr Thr
 340 345 350
 Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser Thr Ala Lys
 355 360 365
 Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380
 Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400
 Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415
 Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430
 Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445
 Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460
 Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480
 Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495
 Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510
 Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525
 Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540
 Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560
 Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575
 Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590
 Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly

595	600	605
Pro Leu Val	Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala	
610	615	620
Ile Gln Gly Val	Ile Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg	
625	630	635
Gly Phe Trp Ala	Ala Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys	640
	645	650
Gly Glu Lys Arg	Lys Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly	655
	660	665
Gly Ala Ala Gln	Thr Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys	670
	675	680
Gln Leu Phe Gly	Ser Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr	685
	690	695
Asp Thr Tyr Ala	Gly Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser	700
705	710	715
Gly Phe Ile Gly	Cys Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His	720
	725	730
Lys Pro Leu Val	Leu Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn	735
	740	745
Asp Leu Lys Thr	Lys Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp	750
	755	760
Gly Asn Asn Ala	Phe Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr	765
	770	775
Pro Glu Tyr Leu	His Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu	780
785	790	795
Asn Leu Thr Tyr	Ile Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu	800
	805	810
Gly Arg Ser Phe	Asp Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile	815
	820	825
Gly Val Lys Phe	Glu Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp	830
	835	840
Leu Thr Leu Ser	Tyr Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys	845
	850	855
Thr Thr Ala Leu	Val Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn	860
865	870	875
Asn Leu Ala Arg	Gln Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala	880
	885	890
Phe Ser Pro Met	Phe Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg	895
	900	905
Gly Ser Ser Arg	Ile Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe	910
	915	920
		925

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCGATTTT	CGCTCTGCGG	ATTTCCTCTA	GTTTTTCTT	TAACATTGCT	CTCAGTCTTC	60
GACACTTCTT	TGAGTGCTAC	TACGATTCTT	TTAACCCAG	AAGATAGTTT	TCATGGAGAT	120
AGTCAGAAATG	CAGAACGTTT	TTATAATGTT	CAAGCTGGGG	ATGTCTATAG	CCTTACTGGT	180

GATGTCTCAA	TATCTAACGT	CGATAACTCT	GCATTAAATA	AAGCCTGCTT	CAATGTGACC	240
TCAGGAAGTG	TGACGTTTCG	AGGAAATCAT	CATGGGTTAT	ATTTTAATAA	TATTTCTCA	300
GGAAGTACAA	AGGAAGGGGC	TGTACTTTGT	TGCCAAGATC	CTCAAGCAAC	GGCACGTTTT	360
TCTGGGTTCT	CCACGCTCTC	TTTTATTTCAG	AGCCCCGGAG	ATATTAAAGA	ACAGGGATGT	420
CTCTATTCAA	AAAATGCAC	TATGCTCTTA	AACAATTATG	TAGTGCGTTT	TGAACAAAAC	480
CAAAGTAAGA	CTAAAGGCGG	AGCTATTAGT	GGGGCGAATG	TTACTATAGT	AGGCAACTAC	540
GATTCCGTCT	CTTTCTATCA	GAATGCAGCC	ACTTTTGGAG	GTGCTATCCA	TTCTTCAGGT	600
CCCCTACAGA	TTGCAGTAAA	TCAGGCAGAG	ATAAGATTG	CACAAAATAC	TGCCAAGAAT	660
GGTTCTGGAG	GGGCTTTGTA	CTCCGATGGT	GATATTGATA	TTGATCAGAA	TGCTTATGTT	720
CTATTTTCGAG	AAAATGAGGC	ATTGACTACT	GCTATAGGTA	AGGGAGGGGC	TGTCTGTTGT	780
CTTCCCCTT	CAGGAAGTAG	TACTCCAGTT	CCTATTGTGA	CTTTCTCTGA	CAATAAACAG	840
TTAGTCTTTG	AAAGAAACCA	TTCCATAATG	GGTGGCGGAG	CCATTTATGC	TAGGAACTT	900
AGCATCTCTT	CAGGAGGTCC	TACTCTATTT	ATCAATAATA	TATCATATGC	AAATTCGCAA	960
AATTTAGGTG	GAGCTATTGC	CATTGATACT	GGAGGGGAGA	TCAGTTTATC	AGCAGAGAAA	1020
GGAACAATTA	CATTCCAAGG	AAACCGGACG	AGCTTACCGT	TTTTGAATGG	CATCCATCTT	1080
TTACAAAATG	CTAAATTCCT	GAAATTACAG	GCGAGAAATG	GATGCTCTAT	AGAATTTTAT	1140
GATCCTATTA	CTTCTGAAGC	AGATGGGTCT	ACCCAATTGA	ATATCAACGG	AGATCCTAAA	1200
AATAAAGAGT	ACACAGGGAC	CATACTCTTT	TCTGGAGAAA	AGAGTCTAGC	AAACGATCCT	1260
AGGGATTTTA	AATCTACAAT	CCCTCAGAAC	GTCAACCTGT	CTGCAGGATA	CTTAGTTATT	1320
AAAGAGGGGG	CCGAAGTCAC	AGTTTCAAAA	TTCACGCAGT	CTCCAGGATC	GCATTTAGTT	1380
TTAGATTTAG	GAACCAAACT	GATAGCCTCT	AAGGAAGACA	TTGCCATCAC	AGGCCTCGCG	1440
ATAGATATAG	ATAGCTTAAG	CTCATCCTCA	ACAGCAGCTG	TTATTAAAGC	AAACACCGCA	1500
AATAAACAGA	TATCCGTGAC	GGACTCTATA	GAACTTATCT	CGCCTACTGG	CAATGCCCTAT	1560
GAAGATCTCA	GAATGAGAAA	TTCACAGACG	TTCCCTCTGC	TCTCTTTAGA	GCCTGGAGCC	1620
GGGGGTAGTG	TGACTGTAAC	TGCTGGAGAT	TTCTTACCGG	TAAGTCCCCA	TTATGGTTTT	1680
CAAGGCAATT	GGAAATTAGC	TTGGACAGGA	ACTGGAAACA	AAGTTGGAGA	ATTCTTCTGG	1740
GATAAAATAA	ATTATAAGCC	TAGACCTGAA	AAAGAAGGAA	ATTTAGTTCC	TAATATCTTG	1800
TGGGGGAATG	CTGTAAATGT	CAGATCCTTA	ATGCAGGTTT	AAGAGACCCA	TGCATCGAGC	1860
TTACAGACAG	ATCGAGGGCT	GTGGATCGAT	GGAATTGGGA	ATTTCTTCCA	TGTATCTGCC	1920
TCCGAAGACA	ATATAAGGTA	CCGTCTAAC	AGCGGTGGAT	ATGTTCTATC	TGTAAATAAT	1980
GAGATCACAC	CTAAGCACTA	TACTTCGATG	GCATTTTCCC	AACCTCTTAG	TAGAGACAAG	2040
GACTATGCGG	TTTCCAACAA	CGAATACAGA	ATGTATTTAG	GATCGTATCT	CTATCAATAT	2100
ACAACCTCCC	TAGGGAATAT	TTTCCGTTAT	GCTTCGCGTA	ACCCTAATGT	AAACGTCGGG	2160
ATTCTCTCAA	GAAGTTTCT	TCAAAATCCT	CTTATGATTT	TTTATTTTTT	GTGTGCTTAT	2220
GGTCATGCCA	CCAATGATAT	GAAAACAGAC	TACGCAAATT	TCCCTATGGT	GAAAAACAGC	2280
TGGAGAAACA	ATTGTTGGGC	TATAGAGTGC	GGAGGGAGCA	TGCCTCTATT	GGTATTTGAG	2340
AACGGAAGAC	TTTTCCAAGG	TGCCATCCCA	TTTATGAAAC	TACAATTAGT	TTATGCTTAT	2400
CAGGGAGATT	TCAAAGAGAC	GACTGCAGAT	GGCCGTAGAT	TTAGTAATGG	GAGTTTAAAC	2460
TCGATTTCTG	TACCTCTAGG	CATACGCTTT	GAGAAGCTGG	CACCTTCTCA	GGATGTACTC	2520
TATGACTTTA	GTTTCTCCTA	TATTCCTGAT	ATTTTCCGTA	AGGATCCCTC	ATGTGAAGCT	2580
GCTCTGGTGA	TTAGCGGAGA	CTCCTGGCTT	GTTCCGGCAG	CACACGTATC	AAGACATGCT	2640
TTTGTAGGGA	GTGGAACGGG	TCGGTATCAC	TTTAACGACT	ATACTGAGCT	CTTATGTCGA	2700
GGAAGTATAG	AATGCCGCCC	CCATGCTAGG	AATTATAATA	TAAACTGTGG	AAGCAAATTT	2760
CGTTTTTAGA	AGGTTTCCAT	TGCCTGTGTG	GTTCCGGATC	TTAACTATAA	ATCCTGGACT	2820
ATGGATCATA	GGCATTGGGT	TTCTCGAACT	TGTGTGGAGA	ATAACGACAT	TTTATATGCA	2880
TAACGGAATA	CTCGTATCAC	CTCAGCCCCT	AGAGACATTC	TTAGGGGTT	CTTTATTTGT	2940
CTAAACTTCG	TATTTTATCG	AGAATCCTTT	ACGTTCTTGG	TTTGCTTGTC	TCCGAGGAGT	3000
TCTCTAACGA	ATCATAGGGA	TTCCAGGGTT	CTGTTCTTGG	AGTCCTTTGG	CA	3052

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Arg	Phe	Ser	Leu	Cys	Gly	Phe	Pro	Leu	Val	Phe	Ser	Leu	Thr	Leu
1				5					10					15	
Leu	Ser	Val	Phe	Asp	Thr	Ser	Leu	Ser	Ala	Thr	Thr	Ile	Ser	Leu	Thr
			20					25					30		
Pro	Glu	Asp	Ser	Phe	His	Gly	Asp	Ser	Gln	Asn	Ala	Glu	Arg	Ser	Tyr
		35				40					45				
Asn	Val	Gln	Ala	Gly	Asp	Val	Tyr	Ser	Leu	Thr	Gly	Asp	Val	Ser	Ile
	50				55						60				
Ser	Asn	Val	Asp	Asn	Ser	Ala	Leu	Asn	Lys	Ala	Cys	Phe	Asn	Val	Thr
65				70					75					80	
Ser	Gly	Ser	Val	Thr	Phe	Ala	Gly	Asn	His	His	Gly	Leu	Tyr	Phe	Asn
			85					90						95	
Asn	Ile	Ser	Ser	Gly	Thr	Thr	Lys	Glu	Gly	Ala	Val	Leu	Cys	Cys	Gln
			100					105					110		
Asp	Pro	Gln	Ala	Thr	Ala	Arg	Phe	Ser	Gly	Phe	Ser	Thr	Leu	Ser	Phe
	115						120					125			
Ile	Gln	Ser	Pro	Gly	Asp	Ile	Lys	Glu	Gln	Gly	Cys	Leu	Tyr	Ser	Lys
	130				135						140				
Asn	Ala	Leu	Met	Leu	Leu	Asn	Asn	Tyr	Val	Val	Arg	Phe	Glu	Gln	Asn
145				150					155					160	
Gln	Ser	Lys	Thr	Lys	Gly	Gly	Ala	Ile	Ser	Gly	Ala	Asn	Val	Thr	Ile
			165					170						175	
Val	Gly	Asn	Tyr	Asp	Ser	Val	Ser	Phe	Tyr	Gln	Asn	Ala	Ala	Thr	Phe
			180					185					190		
Gly	Gly	Ala	Ile	His	Ser	Ser	Gly	Pro	Leu	Gln	Ile	Ala	Val	Asn	Gln
	195						200					205			
Ala	Glu	Ile	Arg	Phe	Ala	Gln	Asn	Thr	Ala	Lys	Asn	Gly	Ser	Gly	Gly
	210					215					220				
Ala	Leu	Tyr	Ser	Asp	Gly	Asp	Ile	Asp	Ile	Asp	Gln	Asn	Ala	Tyr	Val
225				230					235					240	
Leu	Phe	Arg	Glu	Asn	Glu	Ala	Leu	Thr	Thr	Ala	Ile	Gly	Lys	Gly	Gly
			245					250					255		
Ala	Val	Cys	Cys	Leu	Pro	Thr	Ser	Gly	Ser	Ser	Thr	Pro	Val	Pro	Ile
		260					265					270			
Val	Thr	Phe	Ser	Asp	Asn	Lys	Gln	Leu	Val	Phe	Glu	Arg	Asn	His	Ser
	275					280						285			
Ile	Met	Gly	Gly	Gly	Ala	Ile	Tyr	Ala	Arg	Lys	Leu	Ser	Ile	Ser	Ser
	290				295						300				
Gly	Gly	Pro	Thr	Leu	Phe	Ile	Asn	Asn	Ile	Ser	Tyr	Ala	Asn	Ser	Gln
305				310					315					320	
Asn	Leu	Gly	Gly	Ala	Ile	Ala	Ile	Asp	Thr	Gly	Gly	Glu	Ile	Ser	Leu
			325					330					335		
Ser	Ala	Glu	Lys	Gly	Thr	Ile	Thr	Phe	Gln	Gly	Asn	Arg	Thr	Ser	Leu
		340					345					350			
Pro	Phe	Leu	Asn	Gly	Ile	His	Leu	Leu	Gln	Asn	Ala	Lys	Phe	Leu	Lys
	355					360					365				
Leu	Gln	Ala	Arg	Asn	Gly	Cys	Ser	Ile	Glu	Phe	Tyr	Asp	Pro	Ile	Thr
	370				375						380				
Ser	Glu	Ala	Asp	Gly	Ser	Thr	Gln	Leu	Asn	Ile	Asn	Gly	Asp	Pro	Lys
385				390					395					400	
Asn	Lys	Glu	Tyr	Thr	Gly	Thr	Ile	Leu	Phe	Ser	Gly	Glu	Lys	Ser	Leu
			405					410					415		
Ala	Asn	Asp	Pro	Arg	Asp	Phe	Lys	Ser	Thr	Ile	Pro	Gln	Asn	Val	Asn

420	425	430
Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val		
435	440	445
Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly		
450	455	460
Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala		
465	470	475
Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys		
485	490	495
Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu		
500	505	510
Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser		
515	520	525
Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val		
530	535	540
Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe		
545	550	555
Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly		
565	570	575
Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu		
580	585	590
Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asn Val Arg		
595	600	605
Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp		
610	615	620
Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala		
625	630	635
Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu		
645	650	655
Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe		
660	665	670
Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu		
675	680	685
Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu		
690	695	700
Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly		
705	710	715
Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe		
725	730	735
Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala		
740	745	750
Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile		
755	760	765
Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu		
770	775	780
Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr		
785	790	795
Gln Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn		
805	810	815
Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys		
820	825	830
Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile		
835	840	845
Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile		
850	855	860
Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala		
865	870	875
		880

(A) LENGTH: 2526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGAAGATTCT	CACTCCGCTT	TTTATTGATA	TCATTAGTAC	CTACGCTTTC	TATGTCGAAT	60
TTATTAGGAG	CTGCTACTAC	CGAAGAGCTA	TCGGCTAGCA	ATAGCTTCGA	TGGAAGTACA	120
TCAACAACAA	GCTTTTCTAG	TAAAACATCA	TCGGCTACAG	ATGGCACCBA	TTACTGTTTT	180
AAAGATTCTG	TAGTTATAGA	AAATGTACCC	AAAACAGGGG	AAACTCAGTC	TACTAGTTGT	240
TTTAAAAATG	ACGCTGCAGC	TGGAGATCTA	AATTTCTTAG	GAGGGGGATT	TTCTTTCACA	300
TTTAGCAATA	TCGATGCAAC	CACGGCTTCT	GGAGCTGCTA	TTGGAAGTGA	AGCAGCTAAT	360
AAGACAGTCA	CGTTATCAGG	ATTTTCGGCA	CTTTCTTTTC	TTAAATCCCC	AGCAAGTACA	420
GTGACTAATG	GATTGGGAGC	TATCAATGTT	AAAGGGAATT	TAAGCCTATT	GGATAATGAT	480
AAGGTATTGA	TTCAGGACAA	TTTCTCAACA	GGAGATGGCG	GAGCAATTAA	TTGTGCAGGC	540
TCCTTGAAGA	TCGCAAAACAA	TAAGTCCCTT	TCTTTTATTG	GAAATAGTTC	TTCAACACGT	600
GGCGGAGCGA	TTCATACCAA	AAACCTCACA	CTATCTTCTG	GTGGGGAAAC	TCTATTTTCAG	660
GGGAATACAG	CGCCTACGGC	TGCTGGTAAA	GGAGGTGCTA	TCGCGATTGC	AGACTCTGGC	720
ACCCTATCCA	TTTCTGGAGA	CAGTGGCGAC	ATTATCTTTG	AAGGCAATAC	GATAGGAGCT	780
ACAGGAACCG	TCTCTCATAG	TGCTATTGAT	TTAGGAACTA	GCGCTAAGAT	AACTGCGTTA	840
CGTGCTGCGC	AAGGACATAC	GATATACTTT	TATGATCCGA	TTACTGTAAC	AGGATCGACA	900
TCTGTTGCTG	ATGCTCTCAA	TATTAATAGC	CCTGATACTG	GAGATAACAA	AGAGTATACG	960
GGAACCATAG	TCTTTTCTGG	AGAGAAGCTC	ACGGAGGCAG	AAGCTAAAGA	TGAGAAGAAC	1020
CGCACTTCTA	AATTACTTCA	AAATGTTGCT	TTTAAAAATG	GAGCTGTAGT	TTTAAAAGGT	1080
GATGTCGTTT	TAAGTGCGAA	CGGTTTCTCT	CAGGATGCAA	ACTCTAAGTT	GATTATGGAT	1140
TTAGGGACGT	CGTTGGTTGC	AAACACCGAA	AGTATCGAGT	TAACGAATTT	GGAAATTAAT	1200
ATAGACTCTC	TCAGGAACGG	GAAAAAGATA	AAACTCAGTG	CTGCCACAGC	TCAGAAAGAT	1260
ATTCGTATAG	ATCGTCCTGT	TGTACTGGCA	ATTAGCGATG	AGAGTTTTTTA	TCAAAATGGC	1320
TTTTTGAATG	AGGACCATTCT	CTATGATGGG	ATTCTTGAGT	TAGATGCTGG	GAAAAGACATC	1380
GTGATTTCTG	CAGATTCTCG	CAGTATAAAT	GCTGTACAAT	CTCCGTATGG	CTATCAGGGA	1440
AAGTGGAACA	TCAATTGGTC	TACTGATGAT	AAGAAAGCTA	CGGTTTCTTG	GGCAAAGCAA	1500
AGTTTTAATC	CCACTGCTGA	GCAGGAGGCT	CCGTTAGTTC	CTAATCTTCT	TTGGGGTTCT	1560
TTTATAGATG	TTCGTCCCTT	CCAAAATTTT	ATAGAGCTAG	GTAAGTGAAGG	TGCTCCTTAC	1620
GAAAAGAGAT	TTTGGGTTGC	AGGCATTTCC	AATGTTTTGC	ATAGGAGCGG	TCGTGAAAAT	1680
CAAAGGAAAT	TCCGTCATGT	GAGTGGAGGT	GCTGTAGTAG	GTGCTAGCAC	GAGGATGCCG	1740
GGTGGTGATA	CCTTGCTCTCT	GGGTTTTGCT	CAGCTCTTTG	CGCGTGACAA	AGACTACTTT	1800
ATGAATACCA	ATTCGCAAAA	GACCTACGCA	GGATCTTTAC	GTTTGACAGCA	CGATGCTTCC	1860
CTATACTCTG	TGGTGAGTAT	CCTTTTAGGA	GAGGGAGGAC	TCCGCGAGAT	CCTGTTGCCT	1920
TATGTTTTCCA	AGACTCTGCC	GTGCTCTTTT	TATGGGCAGC	TTAGCTACGG	CCATACGGAT	1980
CATCGCATGA	AGACCGAGTC	TCTACCCCCC	CCCCCCCCGA	CGCTCTCGAC	GGATCATACT	2040
TCTTGGGGAG	GATATGCTCTG	GGCTGGAGAG	CTGGGAACTC	GAGTTGCTGT	TGAAAAATACC	2100
AGCGGCAGAG	GATTTTTCCG	AGAGTACACT	CCATTTGTAA	AAGTCCAAGC	TGTTTACTCG	2160
CGCCAAGATA	GCTTTGTTGA	ACTAGGAGCT	ATCAGTCGTG	ATTTTAGTGA	TTCGCATCTT	2220
TATAACCTTG	CGATTCCCTCT	TGGAATCAAG	TTAGAGAAAC	GGTTTGCAGA	GCAATATTAT	2280

CATGTTGTAG	CGATGTATTC	TCCAGATGTT	TGTCGTAGTA	ACCCCAAATG	TACGACTACC	2340
CTACTTTCCA	ACCAAGGGAG	TTGGAAGACC	AAAGGTTTGA	ACTTAGCAAG	ACAGGCTGGT	2400
ATTGTTTCAAG	CCTCAGGTTT	TCGATCTTTG	GGAGCTGCAG	CAGAGCTTTT	CGGGAACCTT	2460
GGCTTTGAAT	GGCGGGGATC	TTCTCGTAGC	TATAATGTAG	ATGCGGGTAG	CAAAATCAAA	2520
TTTTAG						2526

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Lys	Ile	Pro	Leu	Arg	Phe	Leu	Leu	Ile	Ser	Leu	Val	Pro	Thr	Leu
1				5					10					15	
Ser	Met	Ser	Asn	Leu	Leu	Gly	Ala	Ala	Thr	Thr	Glu	Glu	Leu	Ser	Ala
			20					25					30		
Ser	Asn	Ser	Phe	Asp	Gly	Thr	Thr	Ser	Thr	Thr	Ser	Phe	Ser	Ser	Lys
		35				40						45			
Thr	Ser	Ser	Ala	Thr	Asp	Gly	Thr	Asn	Tyr	Val	Phe	Lys	Asp	Ser	Val
	50				55						60				
Val	Ile	Glu	Asn	Val	Pro	Lys	Thr	Gly	Glu	Thr	Gln	Ser	Thr	Ser	Cys
65				70					75						80
Phe	Lys	Asn	Asp	Ala	Ala	Ala	Gly	Asp	Leu	Asn	Phe	Leu	Gly	Gly	Gly
			85					90					95		
Phe	Ser	Phe	Thr	Phe	Ser	Asn	Ile	Asp	Ala	Thr	Thr	Ala	Ser	Gly	Ala
			100					105					110		
Ala	Ile	Gly	Ser	Glu	Ala	Ala	Asn	Lys	Thr	Val	Thr	Leu	Ser	Gly	Phe
	115						120					125			
Ser	Ala	Leu	Ser	Phe	Leu	Lys	Ser	Pro	Ala	Ser	Thr	Val	Thr	Asn	Gly
	130					135					140				
Leu	Gly	Ala	Ile	Asn	Val	Lys	Gly	Asn	Leu	Ser	Leu	Leu	Asp	Asn	Asp
145				150					155					160	
Lys	Val	Leu	Ile	Gln	Asp	Asn	Phe	Ser	Thr	Gly	Asp	Gly	Gly	Ala	Ile
			165						170					175	
Asn	Cys	Ala	Gly	Ser	Leu	Lys	Ile	Ala	Asn	Asn	Lys	Ser	Leu	Ser	Phe
			180					185					190		
Ile	Gly	Asn	Ser	Ser	Ser	Thr	Arg	Gly	Gly	Ala	Ile	His	Thr	Lys	Asn
	195					200						205			
Leu	Thr	Leu	Ser	Ser	Gly	Gly	Glu	Thr	Leu	Phe	Gln	Gly	Asn	Thr	Ala
	210				215						220				
Pro	Thr	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Ala	Ile	Ala	Asp	Ser	Gly
225				230					235					240	
Thr	Leu	Ser	Ile	Ser	Gly	Asp	Ser	Gly	Asp	Ile	Ile	Phe	Glu	Gly	Asn
			245					250					255		
Thr	Ile	Gly	Ala	Thr	Gly	Thr	Val	Ser	His	Ser	Ala	Ile	Asp	Leu	Gly
		260						265					270		
Thr	Ser	Ala	Lys	Ile	Thr	Ala	Leu	Arg	Ala	Ala	Gln	Gly	His	Thr	Ile
	275					280						285			
Tyr	Phe	Tyr	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp
290					295						300				
Ala	Leu	Asn	Ile	Asn	Ser	Pro	Asp	Thr	Gly	Asp	Asn	Lys	Glu	Tyr	Thr

305		310		315		320
Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys						
	325			330		335
Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys						
	340			345		350
Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly						
	355			360		365
Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser						
	370			375		380
Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn						
385		390		395		400
Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr						
	405			410		415
Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser						
	420			425		430
Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr						
	435			440		445
Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala						
	450			455		460
Asp Ser Arg Ser Ile Asn Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly						
465		470		475		480
Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser						
	485			490		495
Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu						
	500			505		510
Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Pro Phe Gln						
	515			520		525
Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe						
	530			535		540
Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn						
545		550		555		560
Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser						
	565			570		575
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu						
	580			585		590
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr						
	595			600		605
Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val						
	610			615		620
Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro						
625		630		635		640
Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr						
	645			650		655
Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro						
	660			665		670
Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala						
	675			680		685
Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly						
	690			695		700
Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser						
705		710		715		720
Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser						
	725			730		735
Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu						
	740			745		750
Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro						
	755			760		765

Asp	Val	Cys	Arg	Ser	Asn	Pro	Lys	Cys	Thr	Thr	Thr	Leu	Leu	Ser	Asn
770						775					780				
Gln	Gly	Ser	Trp	Lys	Thr	Lys	Gly	Ser	Asn	Leu	Ala	Arg	Gln	Ala	Gly
785					790					795					800
Ile	Val	Gln	Ala	Ser	Gly	Phe	Arg	Ser	Leu	Gly	Ala	Ala	Ala	Glu	Leu
				805					810					815	
Phe	Gly	Asn	Phe	Gly	Phe	Glu	Trp	Arg	Gly	Ser	Ser	Arg	Ser	Tyr	Asn
			820					825					830		
Val	Asp	Ala	Gly	Ser	Lys	Ile	Lys	Phe							
835							840								

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAGTCTT	CTTTCCCCAA	GTTTGTATTT	TCTACATTTG	CTATTTTCCC	TTTGTCTATG	60
ATTGCTACCG	AGACAGTTTT	GGATTCAAGT	GCGAGTTTCG	ATGGGAATAA	AAATGGTAAT	120
TTTTCAAGTTC	GTGAGAGTCA	GGAAGATGCT	GGAAGTACCT	ACCTATTTAA	GGGAAATGTC	180
ACTCTAGAAA	ATATTCCTGG	AACAGGCACA	GCAATCACAA	AAAGCTGTTT	TAACAACACT	240
AAGGGCGATT	TGACTTTCAC	AGGTAACGGG	AACTCTCTAT	TGTTCCAAAC	GGTGGATGCA	300
GGGACTGTAG	CAGGGGCTGC	TGTTAACAGC	AGCGTGGTAG	ATAAATCTAC	CACGTTTATA	360
GGGTTTTCTT	CGCTATCTTT	TATTGCGTCT	CCTGGAAGTT	CGATAACTAC	CGGCAAAGGA	420
GCCGTTAGCT	GCTCTACGGG	TAGCTTGAAG	TTTGACAAAA	ATGTCAGTTT	GCTCTTCAGC	480
AAAAACTTTT	CAACGGATAA	TGGCGGTGCT	ATCACCAGCA	AACTCTTTC	ATTAACAGGG	540
ACTACAATGT	CAGCTCTGTT	TTCTGAAAAT	ACCTCCTCAA	AGAAAGGCGG	AGCCATTGAG	600
ACTTCCGATG	CCCTTACCAT	TACTGGAAAC	CAAGGGGAAG	TCTCTTTTTC	TGACAATACT	660
TCTTCGGATT	CTGGAGCTGC	AATTTTTTACA	GAAGCCTCGG	TGACTATTTT	TAATAATGCT	720
AAAGTTTCCT	TTATTGACAA	TAAGGTCACA	GGAGCGAGCT	CCTCAACAAC	GGGGGATATG	780
TCAGGAGGTG	CTATCTGTGC	TTATAAAACT	AGTACAGATA	CTAAGGTCAC	CCTCACTGGA	840
AATCAGATGT	TACTCTTCAG	CAACAATACA	TCGACAACAG	CGGGAGGAGC	TATCTATGTG	900
AAAAAGCTCG	AACTGGCTTC	CGGAGGACTT	ACCCTATTCA	GTAGAAATAG	TGTCAATGGA	960
GGTACAGCTC	CTAAAGGTGG	AGCCATAGCT	ATCGAAGATA	GTGGGGAATT	GAGTTTATCC	1020
GCCGATAGTG	GTGACATTGT	CTTTTTAGGG	AATACAGTCA	CTTCTACTAC	TCCTGGGACG	1080
AATAGAAGTA	GTATCGACTT	AGGAACGAGT	GCAAAGATGA	CAGCTTTGCG	TTCTGCTGCT	1140
GGTAGAGCCA	TCTACTTCTA	TGATCCCAT	ACTACAGGAT	CTTCCACAAC	AGTTACAGAT	1200
GTCTTAAAG	TTAATGAGAC	TCCGGCAGAT	TCTGCACTAC	AATATACAGG	GAACATCATC	1260
TTCACAGGAG	AAAAGTTATC	AGAGACAGAG	GCCGCAGATT	CTAAAAATCT	TACTTCGAAG	1320
CTACTACAGC	CTGTAACCTC	TTCAGGAGGT	ACTCTATCTT	TAAAACATGG	AGTGACTCTG	1380
CAGACTCAGG	CATTCACTCA	ACAGGCAGAT	TCTCGTCTCG	AAATGGACGT	AGGAACTACT	1440
CTAGAACCTG	CTGATACTAG	CACCATAAAC	AATTTGGTCA	TTAACATCAG	TTCTATAGAC	1500
GGTGCAAAGA	AGGCAAAAAT	AGAAACCAAA	GCTACGTCAA	AAAATCTGAC	TTTATCTGGA	1560
ACCATCACTT	TATTGGACCC	GACGGGCACG	TTTTATGAAA	ATCATAGTTT	AAGAAATCCT	1620
CAGTCCTACG	ACATCTTAGA	GCTCAAAGCT	TCTGGAAGT	TAACAAGCAC	CGCAGTGACT	1680
CCAGATCCTA	TAATGGGTGA	GAAATTCCAT	TACGGCTATC	AGGGAAGTGG	GGGCCCAATT	1740
GTTTGGGGGA	CAGGGGCTTC	TACGACTGCA	ACCTTCAACT	GGACTAAAAC	TGGCTATATT	1800
CCTAATCCCG	AGCGTATCGG	CTCTTTAGTC	CCTAATAGCT	TATGGAATGC	ATTTATAGAT	1860
ATTAGCTCTC	TCCATTATCT	TATGGAGACT	GCAAACGAAG	GGTTGCAGGG	AGACCGTGCT	1920
TTTTGGTGTG	CTGGATTATC	TAAGTTCTTC	CATAAGGATA	GTACAAAAAC	ACGACGCGGG	1980
TTTCGCCATT	TGAGTGGCGG	TTATGTCATA	GGAGGAAACC	TACATACTTG	TTCAGATAAG	2040

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ATTCTTAGTG CTGCATTTTG TCAGCTCTTT GGAAGAGATA GAGACTACTT TGTAGCTAAG 2100
AATCAAGGTA CAGTCTACGG AGGAACTCTC TATTACCAGC ACAACGAAAC CTATATCTCT 2160
CTTCCTTGCA AACTACGGCC TTGTTCTGTTG TCTTATGTTT CTACAGAGAT TCCTGTTCTC 2220
TTTTTCAGGAA ACCTTAGCTA CACCCATACG GATAACGATC TGAAAACCAA GTATACAACA 2280
TATCCTACTG TTAAAGGAAG CTGGGGGAAT GATAGTTTCG CTTTAGAATT CGGTGGAAGA 2340
GCTCCGATTT GCTTAGATGA AAGTGCTCTA TTTGAGCAGT ACATGCCCTT CATGAAATTG 2400
CAGTTTGTCT ATGCACATCA GGAAGGTTTT AAAGAACAGG GAACAGAAGC TCGTGAATTT 2460
GGAAGTAGCC GTCTTGTAAG TCTTGCCTTA CCTATCGGGA TCCGATTTGA TAAGGAATCA 2520
GACTGCCAAG ATGCAACGTA CAATCTAAT CTTGGTTATA CTGTGGATCT TGTTCGTAGT 2580
AACCCCGACT GTACGACAAC ACTGCGAATT AGCGGTGATT CTTGGAAAAC CTTCCGTACG 2640
AATTTGGCAA GACAAGCTTT AGTCCTTCGT GCAGGGAACC ATTTTGTCTT TAACTCAAAT 2700
TTTGAAGCCT TTAGCCAATT TTCTTTTGAA TTGCGTGGGT CATCTCGCAA TTACAATGTA 2760
GACTTAGGAG CAAAATACCA ATTCTAA 2787

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Lys Ser Ser Phe Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe
 1           5           10           15
Pro Leu Ser Met Ile Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser
 20           25           30
Phe Asp Gly Asn Lys Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu
 35           40           45
Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn
 50           55           60
Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr
 65           70           75           80
Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln
 85           90           95
Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val
100           105           110
Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile
115           120           125
Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys
130           135           140
Ser Thr Gly Ser Leu Lys Phe Asp Lys Asn Val Ser Leu Leu Phe Ser
145           150           155           160
Lys Asn Phe Ser Thr Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu
165           170           175
Ser Leu Thr Gly Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser
180           185           190
Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr
195           200           205
Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser
210           215           220
Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala
225           230           235           240
Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr

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					245					250					255		
Thr	Gly	Asp	Met	Ser	Gly	Gly	Ala	Ile	Cys	Ala	Tyr	Lys	Thr	Ser	Thr		
			260					265					270				
Asp	Thr	Lys	Val	Thr	Leu	Thr	Gly	Asn	Gln	Met	Leu	Leu	Phe	Ser	Asn		
		275					280					285					
Asn	Thr	Ser	Thr	Thr	Ala	Gly	Gly	Ala	Ile	Tyr	Val	Lys	Lys	Leu	Glu		
		290				295					300						
Leu	Ala	Ser	Gly	Gly	Leu	Thr	Leu	Phe	Ser	Arg	Asn	Ser	Val	Asn	Gly		
305					310					315					320		
Gly	Thr	Ala	Pro	Lys	Gly	Gly	Ala	Ile	Ala	Ile	Glu	Asp	Ser	Gly	Glu		
				325					330					335			
Leu	Ser	Leu	Ser	Ala	Asp	Ser	Gly	Asp	Ile	Val	Phe	Leu	Gly	Asn	Thr		
				340				345					350				
Val	Thr	Ser	Thr	Thr	Pro	Gly	Thr	Asn	Arg	Ser	Ser	Ile	Asp	Leu	Gly		
		355					360					365					
Thr	Ser	Ala	Lys	Met	Thr	Ala	Leu	Arg	Ser	Ala	Ala	Gly	Arg	Ala	Ile		
		370				375					380						
Tyr	Phe	Tyr	Asp	Pro	Ile	Thr	Thr	Gly	Ser	Ser	Thr	Thr	Val	Thr	Asp		
385				390						395					400		
Val	Leu	Lys	Val	Asn	Glu	Thr	Pro	Ala	Asp	Ser	Ala	Leu	Gln	Tyr	Thr		
				405					410					415			
Gly	Asn	Ile	Ile	Phe	Thr	Gly	Glu	Lys	Leu	Ser	Glu	Thr	Glu	Ala	Ala		
			420					425					430				
Asp	Ser	Lys	Asn	Leu	Thr	Ser	Lys	Leu	Leu	Gln	Pro	Val	Thr	Leu	Ser		
		435					440					445					
Gly	Gly	Thr	Leu	Ser	Leu	Lys	His	Gly	Val	Thr	Leu	Gln	Thr	Gln	Ala		
		450				455					460						
Phe	Thr	Gln	Gln	Ala	Asp	Ser	Arg	Leu	Glu	Met	Asp	Val	Gly	Thr	Thr		
465				470						475					480		
Leu	Glu	Pro	Ala	Asp	Thr	Ser	Thr	Ile	Asn	Asn	Leu	Val	Ile	Asn	Ile		
				485					490					495			
Ser	Ser	Ile	Asp	Gly	Ala	Lys	Lys	Ala	Lys	Ile	Glu	Thr	Lys	Ala	Thr		
			500					505					510				
Ser	Lys	Asn	Leu	Thr	Leu	Ser	Gly	Thr	Ile	Thr	Leu	Leu	Asp	Pro	Thr		
		515					520					525					
Gly	Thr	Phe	Tyr	Glu	Asn	His	Ser	Leu	Arg	Asn	Pro	Gln	Ser	Tyr	Asp		
		530				535					540						
Ile	Leu	Glu	Leu	Lys	Ala	Ser	Gly	Thr	Val	Thr	Ser	Thr	Ala	Val	Thr		
545				550						555					560		
Pro	Asp																

Val Tyr Gly Gly Thr Leu Tyr Tyr Gln His Asn Glu Thr Tyr Ile Ser
 705 710 715 720
 Leu Pro Cys Lys Leu Arg Pro Cys Ser Leu Ser Tyr Val Pro Thr Glu
 725 730 735
 Ile Pro Val Leu Phe Ser Gly Asn Leu Ser Tyr Thr His Thr Asp Asn
 740 745 750
 Asp Leu Lys Thr Lys Tyr Thr Thr Tyr Pro Thr Val Lys Gly Ser Trp
 755 760 765
 Gly Asn Asp Ser Phe Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys
 770 775 780
 Leu Asp Glu Ser Ala Leu Phe Glu Gln Tyr Met Pro Phe Met Lys Leu
 785 790 795 800
 Gln Phe Val Tyr Ala His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu
 805 810 815
 Ala Arg Glu Phe Gly Ser Ser Arg Leu Val Asn Leu Ala Leu Pro Ile
 820 825 830
 Gly Ile Arg Phe Asp Lys Glu Ser Asp Cys Gln Asp Ala Thr Tyr Asn
 835 840 845
 Leu Thr Leu Gly Tyr Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys
 850 855 860
 Thr Thr Thr Leu Arg Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr
 865 870 875 880
 Asn Leu Ala Arg Gln Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys
 885 890 895
 Phe Asn Ser Asn Phe Glu Ala Phe Ser Gln Phe Ser Phe Glu Leu Arg
 900 905 910
 Gly Ser Ser Arg Asn Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2757 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGATCGT	CTTTTTCCTT	GTTATTAATA	TCTTCATCTC	TAGCCTTTCC	TCTCTTAATG	60
AGTGTTTCTG	CAGATGCTGC	CGATCTCACA	TTAGGGAGTC	GTGACAGTTA	TAATGGTGAT	120
ACAAGCACCA	CAGAATTTAC	TCCTAAAGCG	GCAACTTCTG	ATGCTAGTGG	CACGACCTAT	180
ATTCTCGATG	GGGATGTCTC	GATAAGCCAA	GCAGGGAAAC	AAACGAGCTT	AACCACAAGT	240
TGTTTTTCTA	ACACTGCAGG	AAATCTTACC	TTCTTAGGGA	ACGGATTTC	TCTTCATTTT	300
GACAATATTA	TTTCGTCTAC	TGTTGCAGGT	GTTGTTGTTA	GCAATACAGC	AGCTTCTGGG	360
ATTACGAAAT	TCTCAGGATT	TTCAACTCTT	CGGATGCTTG	CAGCTCCTAG	GACCACAGGT	420
AAAGGAGCCA	TTAAATTTAC	CGATGGTCTG	GTGTTTGAGA	GTATAGGGAA	TCTTGACCAA	480
AATGAAAATG	CCTCTAGTGA	AAATGGGGGA	GCCATCAATA	CGAAGACTTT	GTCTTTGACT	540
GGGAGTACGC	GGTTTGATGC	GTTCTTGTC	AATAGCTCGT	CGCAACAAGG	GGGAGCGATC	600
TATGCTTCTG	GTGACTCTGT	GATTTCTGAG	AATGCAGGAA	TCTTGAGCTT	CGGAAACAAC	660
AGTGCGACAA	CATCAGGAGG	CGCGATCTCT	GCTGAAGGGA	ACCTTGTGAT	CTCCAATAAC	720
CAAAATATCT	TTTTCGATGG	CTGCAAAGCA	ACTACAAATG	GCGGAGCTAT	TGATTGTAAC	780
AAAGCAGGGG	CGAACCCAGA	CCCTATCTTG	ACTCTTTCAG	GAAATGAGAG	CCTGCATTTT	840
CTGAATAACA	CAGCAGGAAA	TAGTGGAGGT	GCGATTTATA	CCAAAAAATT	GGTGTATATCC	900
TCAGGACGAG	GAGGAGTGTT	ATTTTCTAAC	AACAAAGCTG	CGAATGCTAC	TCCTAAAGGA	960

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GGGGCAATTG CGATTCTAGA TTCTGGAGAG ATTAGCATTT CTGCAGATCT CGGCAATATC 1020
ATTTTCGAGG GCAATACTAC GAGCACTACA GGAAGTCCTG CGAGTGTGAC CAGAAATGCT 1080
ATAGATCTTG CATCGAATGC AAAATTTTTTA AATCTCCGAG CGACTCGGGG AAATAAAGTT 1140
ATTTTCTATG ATCCTATCAC GAGCTCAGGA GCTACTGATA AGCTCTCTTT GAATAAAGCT 1200
GACGCAGGAT CTGGAAATAC CTATGAAGGC TACATCGTTT TCTCTGGAGA GAAACTCTCA 1260
GAAGAGGAAC TTAAGAAACC TGACAATCTG AAGTCTACAT TTACACAGGC TGTAGAGCTT 1320
GCTGCAGGTG CCTTAGTATT GAAAGATGGA GTGACTGTAG TTGCAAATAC TATAACGCAG 1380
GTCGAGGGAT CGAAAGTCGT TATGGATGGA GGGACTACTT TTGAGGCAAG CGCTGAGGGG 1440
GTCACCTCTCA ATGGCCTAGC CATTAAATATA GATTCCCTTAG ATGGGACAAA TAAAGCTATC 1500
ATTAAGGCGA CGGCAGCAAG TAAGGATGTT GCCTTATCAG GGCCTATCAT GCTTGTAGAT 1560
GCTCAGGGGA ACTATTATGA GCATCATAAT CTCAGTCAAC AGCAGGTCTT TCCTTTAATA 1620
GAGCTTTCTG CACAAGGAAC GATGACTACT ACAGATATCC CCGATACCCC AATTCTAAT 1680
ACTACGAATC ACTATGGGTA TCAAGGAACT GGAATAATTG TTTGGGTCGA CGATGCAACT 1740
GCAAAAACAA AAAATGCTAC CTTAAGTTGG ACTAAAACAG GATACAAGCC GAATCCAGAA 1800
CGTCAGGGAC CTTTGGTTCC TAATAGCCTG TGGGGTTCTT TTGTCGATGT CCGCTCCATT 1860
CAGAGCCTCA TGGACCGGAG CACAAGTTCTG TTATCTTCGT CAACAAATTT GTGGGTATCA 1920
GGAATCGCGG ACTTTTTCGA TGAAGATCAG AAAGGAAACC AACGTAGTTA TCGTCATTCT 1980
AGCGCGGGTT ATGCATTAGG AGGAGGATTC TTCACGGCTT CTGAAAATTT CTTTAATTTT 2040
GCTTTTTGTC AGCTTTTTGG CTACGACAAG GACCATCTTG TGGCTAAGAA CCATACCCAT 2100
GTATATGCAG GGGCAATGAG TTACCGACAC CTCGGAGAGT CTAAGACCCT CGCTAAGATT 2160
TTGTCAGGAA ATTCTGACTC CCTACCTTTT GTCTTCAATG CTCGGTTTGC TTATGGCCAT 2220
ACCGACAATA ACATGACCAC AAAGTACACT GGCTATTCTC CTGTTAAGGG AAGCTGGGGA 2280
AATGATGCCT TCGGTATAGA ATGTGGAGGA GCTATCCCGG TAGTTGCTTC AGGACGTCGG 2340
TCTTGGGTGG ATACCCACAC GCCATTCTA AACCTAGAGA TGATCTATGC ACATCAGAAT 2400
GACTTTAAGG AAAACGGCAC AGAAGGCCGT TCTTCCGATA GTGAAGACCT CTTCAATCTA 2460
GCGGTTCTCTG TAGGGATAAA ATTTGAGAAA TTCTCCGATA AGTCTACGTA TGATCTCTCC 2520
ATAGCTTACG TTCCCAGTGT GATTCGTAAT GATCCAGGCT GCACGACAAC TCTTATGGTT 2580
TCTGGGGATT CTTGGTCGAC ATGTGGTACA AGCTTGTCTA GACAAGCTCT TCTTGTACGT 2640
GCTGGAAATC ATCATGCCTT TGCTTCAAAC TTTGAAGTTT TCAGTCAGTT TGAAGTCGAG 2700
TTGCGAGGTT CTTCTCGTAG CTATGCTATC GATCTTGGAG GAAGATTCGG ATTTTAA 2757

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Met Arg Ser Ser Phe Ser Leu Leu Leu Ile Ser Ser Ser Leu Ala Phe
 1           5           10           15
Pro Leu Leu Met Ser Val Ser Ala Asp Ala Ala Asp Leu Thr Leu Gly
 20           25           30
Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr Thr Glu Phe Thr Pro
 35           40           45
Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr Tyr Ile Leu Asp Gly
 50           55           60
Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr Ser Leu Thr Thr Ser
 65           70           75           80
Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe Leu Gly Asn Gly Phe
 85           90           95
Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr Val Ala Gly Val Val
100           105           110

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Val	Ser	Asn	Thr	Ala	Ala	Ser	Gly	Ile	Thr	Lys	Phe	Ser	Gly	Phe	Ser	115	120	125
Thr	Leu	Arg	Met	Leu	Ala	Ala	Pro	Arg	Thr	Thr	Gly	Lys	Gly	Ala	Ile	130	135	140
Lys	Ile	Thr	Asp	Gly	Leu	Val	Phe	Glu	Ser	Ile	Gly	Asn	Leu	Asp	Gln	145	150	155
Asn	Glu	Asn	Ala	Ser	Ser	Glu	Asn	Gly	Gly	Ala	Ile	Asn	Thr	Lys	Thr	165	170	175
Leu	Ser	Leu	Thr	Gly	Ser	Thr	Arg	Phe	Val	Ala	Phe	Leu	Gly	Asn	Ser	180	185	190
Ser	Ser	Gln	Gly	Gly	Ala	Ile	Tyr	Ala	Ser	Gly	Asp	Ser	Val	Ile		195	200	205
Ser	Glu	Asn	Ala	Gly	Ile	Leu	Ser	Phe	Gly	Asn	Asn	Ser	Ala	Thr	Thr	210	215	220
Ser	Gly	Gly	Ala	Ile	Ser	Ala	Glu	Gly	Asn	Leu	Val	Ile	Ser	Asn	Asn	225	230	235
Gln	Asn	Ile	Phe	Phe	Asp	Gly	Cys	Lys	Ala	Thr	Thr	Asn	Gly	Gly	Ala	245	250	255
Ile	Asp	Cys	Asn	Lys	Ala	Gly	Ala	Asn	Pro	Asp	Pro	Ile	Leu	Thr	Leu	260	265	270
Ser	Gly	Asn	Glu	Ser	Leu	His	Phe	Leu	Asn	Asn	Thr	Ala	Gly	Asn	Ser	275	280	285
Gly	Gly	Ala	Ile	Tyr	Thr	Lys	Lys	Leu	Val	Leu	Ser	Ser	Gly	Arg	Gly	290	295	300
Gly	Val	Leu	Phe	Ser	Asn	Asn	Lys	Ala	Ala	Asn	Ala	Thr	Pro	Lys	Gly	305	310	315
Gly	Ala	Ile	Ala	Ile	Leu	Asp	Ser	Gly	Glu	Ile	Ser	Ile	Ser	Ala	Asp	325	330	335
Leu	Gly	Asn	Ile	Ile	Phe	Glu	Gly	Asn	Thr	Thr	Ser	Thr	Thr	Gly	Ser	340	345	350
Pro	Ala	Ser	Val	Thr	Arg	Asn	Ala	Ile	Asp	Leu	Ala	Ser	Asn	Ala	Lys	355	360	365
Phe	Leu	Asn	Leu	Arg	Ala	Thr	Arg	Gly	Asn	Lys	Val	Ile	Phe	Tyr	Asp	370	375	380
Pro	Ile	Thr	Ser	Ser	Gly	Ala	Thr	Asp	Lys	Leu	Ser	Leu	Asn	Lys	Ala	385	390	395
Asp	Ala	Gly	Ser	Gly	Asn	Thr	Tyr	Glu	Gly	Tyr	Ile	Val	Phe	Ser	Gly	405	410	415
Glu	Lys	Leu	Ser	Glu	Glu	Glu	Leu	Lys	Lys	Pro	Asp	Asn	Leu	Lys	Ser	420	425	430
Thr	Phe	Thr	Gln	Ala	Val	Glu	Leu	Ala	Ala	Gly	Ala	Leu	Val	Leu	Lys	435	440	445
Asp	Gly	Val	Thr	Val	Val	Ala	Asn	Thr	Ile	Thr	Gln	Val	Glu	Gly	Ser	450	455	460
Lys	Val	Val	Met	Asp	Gly	Gly	Thr	Thr	Phe	Glu	Ala	Ser	Ala	Glu	Gly	465	470	475
Val	Thr	Leu	Asn	Gly	Leu	Ala	Ile	Asn	Ile	Asp	Ser	Leu	Asp	Gly	Thr	485	490	495
Asn	Lys	Ala	Ile	Ile	Lys	Ala	Thr	Ala	Ala	Ser	Lys	Asp	Val	Ala	Leu	500	505	510
Ser	Gly	Pro	Ile	Met	Leu	Val	Asp	Ala	Gln	Gly	Asn	Tyr	Tyr	Glu	His	515	520	525
His	Asn	Leu	Ser	Gln	Gln	Gln	Val	Phe	Pro	Leu	Ile	Glu	Leu	Ser	Ala	530	535	540
Gln	Gly	Thr	Met	Thr	Thr	Thr	Asp	Ile	Pro	Asp	Thr	Pro	Ile	Leu	Asn	545	550	555
Thr	Thr	Asn	His	Tyr	Gly	Tyr	Gln	Gly	Thr	Gly	Ile	Ile	Val	Trp	Val	560		

										565											570											575
Asp	Asp	Ala	Thr	Ala	Lys	Thr	Lys	Asn	Ala	Thr	Leu	Thr	Trp	Thr	Lys																	
										580											585											590
Thr	Gly	Tyr	Lys	Pro	Asn	Pro	Glu	Arg	Gln	Gly	Pro	Leu	Val	Pro	Asn																	
										595											600											605
Ser	Leu	Trp	Gly	Ser	Phe	Val	Asp	Val	Arg	Ser	Ile	Gln	Ser	Leu	Met																	
										610											615											620
Asp	Arg	Ser	Thr	Ser	Ser	Leu	Ser	Ser	Ser	Thr	Asn	Leu	Trp	Val	Ser																	
										625											630											635
Gly	Ile	Ala	Asp	Phe	Leu	His	Glu	Asp	Gln	Lys	Gly	Asn	Gln	Arg	Ser																	
										645											650											655
Tyr	Arg	His	Ser	Ser	Ala	Gly	Tyr	Ala	Leu	Gly	Gly	Gly	Phe	Phe	Thr																	
										660											665											670
Ala	Ser	Glu	Asn	Phe	Phe	Asn	Phe	Ala	Phe	Cys	Gln	Leu	Phe	Gly	Tyr																	
										675											680											685
Asp	Lys	Asp	His	Leu	Val	Ala	Lys	Asn	His	Thr	His	Val	Tyr	Ala	Gly																	
										690											695											700
Ala	Met	Ser	Tyr	Arg	His	Leu	Gly	Glu	Ser	Lys	Thr	Leu	Ala	Lys	Ile																	
										705											710											715
Leu	Ser	Gly	Asn	Ser	Asp	Ser	Leu	Pro	Phe	Val	Phe	Asn	Ala	Arg	Phe																	
										725											730											735
Ala	Tyr	Gly	His	Thr	Asp	Asn	Asn	Met	Thr	Thr	Lys	Tyr	Thr	Gly	Tyr																	
										740											745											750
Ser	Pro	Val	Lys	Gly	Ser	Trp	Gly	Asn	Asp	Ala	Phe	Gly	Ile	Glu	Cys																	
										755											760											765
Gly	Gly	Ala	Ile	Pro	Val	Val	Ala	Ser	Gly	Arg	Arg	Ser	Trp	Val	Asp																	
										770											775											780
Thr	His	Thr	Pro	Phe	Leu	Asn	Leu	Glu	Met	Ile	Tyr	Ala	His	Gln	Asn																	
										785											790											795
Asp	Phe	Lys	Glu	Asn	Gly	Thr	Glu	Gly	Arg	Ser	Phe	Gln	Ser	Glu	Asp																	
										805											810											815
Leu	Phe	Asn	Leu	Ala	Val	Pro	Val	Gly	Ile	Lys	Phe	Glu	Lys	Phe	Ser																	
										820											825											830
Asp	Lys	Ser	Thr	Tyr	Asp	Leu	Ser	Ile	Ala	Tyr	Val	Pro	Asp	Val	Ile																	
										835											840											845
Arg	Asn	Asp	Pro	Gly	Cys	Thr	Thr	Thr	Leu	Met	Val	Ser	Gly	Asp	Ser																	
										850											855											860
Trp	Ser	Thr	Cys	Gly	Thr	Ser	Leu	Ser	Arg	Gln	Ala	Leu	Leu	Val	Arg																	
										865											870											875
Ala	Gly	Asn	His	His	Ala	Phe	Ala	Ser	Asn	Phe	Glu	Val	Phe	Ser	Gln																	
										885											890											895
Phe	Glu	Val	Glu	Leu	Arg	Gly	Ser	Ser	Arg	Ser	Tyr	Ala	Ile	Asp	Leu																	
										900											905											910
Gly	Gly	Arg	Phe	Gly	Phe																											
										915																						

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGAAATCCT	CTCTTCATTG	GTTTGTAATC	TCGTCATCTT	TAGCACTTCC	CTTGTCACCTA	60
AATTTCTCTG	CGTTTGCTGC	TGTTGTTGAA	ATCAATCTAG	GACCTACCAA	TAGCTTCTCT	120
GGACCAGGAA	CCTACACTCC	TCCAGCCCAA	ACAACAAATG	CAGATGGAAC	TATCTATAAT	180
CTAACAGGGG	ATGTCTCAAT	CACCAATGCA	GGATCTCCGA	CAGCTCTAAC	CGCTTCCTGC	240
TTTAAAGAAA	CTACTGGGAA	TCTTTCTTTC	CAAGGCCACG	GCTACCAATT	TCTCCTACAA	300
AATATCGATG	CGGGAGCGAA	CTGTACCTTT	ACCAATACAG	CTGCAAATAA	GCTTCTCTCC	360
TTTTTCAGGAT	TCTCCTATTT	GTCACATAA	CAAACCACGA	ATGCTACCAC	AGGAACAGGA	420
GCCATCAAGT	CCACAGGAGC	TTGTTCTATT	CAGTCGAAC	ATAGTTGCTA	CTTTGGCCAA	480
AACTTTTCTA	ATGACAATGG	AGGCGCCCTC	CAAGGCAGCT	CTATCAGTCT	ATCGCTAAAC	540
CCCAACCTAA	CGTTTGCCAA	AAACAAAGCA	ACGCAAAAAG	GGGGTGCCCT	CTATTCCACG	600
GGAGGGATTA	CAATTAACAA	TACGTTAAAC	TCAGCATCAT	TTTCTGAAAA	TACCGCGGCG	660
AACAATGGCG	GAGCCATTTA	CACGGAAGCT	ACAGTTTTAA	TTAGCAGCAA	CAAAGCAATT	720
AGCTTTATAA	ACAATAGTGT	GACCGCAACC	TCAGCTACAG	GGGGAGCCAT	TTACTGTAGT	780
AGTACATCAG	CCCCCAAACC	AGTCTTAACT	CTATCAGACA	ACGGGGAAC	GAACCTTTATA	840
GGAAATACAG	CAATTACTAG	TGGTGGGGCG	ATTTATACTG	ACAATCTAGT	TCTTTCTTCT	900
GGAGGACCTA	CGCTTTTTAA	AAACAACCTCT	GCTATAGATA	CTGCAGCTCC	CTTAGGAGGA	960
GCAATTGCGA	TTGCTGACTC	TGGATCTTTG	AGTCTTTCGG	CTCTTGGTGG	AGACATCACT	1020
TTTGAAGGAA	ACACAGTAGT	CAAAGGAGCT	TCTTCGAGTC	AGACCACTAC	CAGAAATTCT	1080
ATTAACATCG	GAAACACCAA	TGCTAAGATT	GTACAGCTGC	GAGCCTCTCA	AGGCAATACT	1140
ATCTACTTCT	ATGATCCTAT	AACAACCTAAC	CATACTGCAG	CTCTCTCAGA	TGCTCTAAAC	1200
TTAAATGGTC	CTGACCTTGC	AGGGAATCCT	GCATATCAAG	GAACCATCGT	ATTTTCTGGA	1260
GAGAAGCTCT	CGGAAGCAGA	AGCTGCAGAA	GCTGATAATC	TCAAATCTAC	AATTCAGCAA	1320
CCTCTAACTC	TTGCGGGAGG	GCAACTCTCT	CTTAAATCAG	GAGTCACTCT	AGTTGCTAAG	1380
TCCTTTTCGC	AATCTCCGGG	CTCTACCCTC	CTCATGGATG	CAGGGACCAC	ATTAGAAACC	1440
GCTGATGGGA	TCACTATCAA	TAATCTTGTT	CTCAATGTAG	ATTCTTTAAA	AGAGACCAAG	1500
AAGGCTACGC	TAAAAGCAAC	ACAAGCAAGT	CAGACAGTCA	CTTTATCTGG	ATCGCTCTCT	1560
CTTGATAGATC	CTTCTGGAAA	TGTCTACGAA	GATGTCTCTT	GGAATAACCC	TCAAGTCTTT	1620
TCTTGCTCTCA	CTCTTACTGC	TGACGACCCC	GCGAATATTTC	ACATCACAGA	CTTAGCTGCT	1680
GATCCCCTAG	AAAAAAATCC	TATCCATTGG	GGATACCAAG	GGAATTGGGC	ATTATCTTGG	1740
CAAGAGGATA	CTGCGACTAA	ATCCAAAGCA	GCGACTCTTA	CCTGGACAAA	AACAGGATAC	1800
AATCCGAATC	CTGAGCGTCG	TGGAACCTTA	GTTGCTAACA	CGCTATGGGG	ATCCTTTGTT	1860
GATGTGCGCT	CCATACAACA	GCTTGTAGCC	ACTAAAGTAC	GCCAATCTCA	AGAAACTCGC	1920
GGCATCTGGT	GTGAAGGGAT	CTCGAACTTC	TTCCATAAAG	ATAGCACGAA	GATAAATAAA	1980
GGTTTTCGCC	ACATAAGTGC	AGGTTATGTT	GTAGGAGCGA	CTACAACATT	AGCTTCTGAT	2040
AATCTTATCA	CTGCAGCCTT	CTGCCAATTA	TTCCGGGAAAG	ATAGAGATCA	CTTTATAAAT	2100
AAAAATAGAG	CTTCTGCCTA	TGCAGCTTCT	CTCCATCTCC	AGCATCTAGC	GACCTTGTCT	2160
TCTCCAAGCT	TGTTACGCTA	CCTTCCTGGA	TCTGAAAGTG	AGCAGCCTGT	CCTCTTTGAT	2220
GCTCAGATCA	GCTATATCTA	TAGTAAAAAT	ACTATGAAAA	CCTATTACAC	CCAAGCACCA	2280
AAGGGAGAGA	GCTCGTGGTA	TAATGACGGT	TGCGCTCTGG	AACTTGCGAG	CTCCCTACCA	2340
CACACTGCTT	TAAGCCATGA	GGGTCTCTTC	CACGCGTATT	TTCTTTTCAT	CAAAGTAGAA	2400
GCTTCGTACA	TACACCAAGA	TAGCTTCAAA	GAACGTAATA	CTACCTTGGT	ACGATCTTTC	2460
GATAGCGGTG	ATTTAATTAA	CGTCTCTGTG	CCTATTGGAA	TTACCTTCGA	GAGATTCTCG	2520
AGAAACGAGC	GTGCGTCTTA	CGAAGCTACT	GTCATCTACG	TTGCCGATGT	CTATCGTAAG	2580
AATCCTGACT	GCACGACAGC	TCTCCTAATC	AACAATACCT	CGTGGAAC	TACAGGAACG	2640
AATCTCTCAA	GACAAGCTGG	TATCGGAAGA	GCAGGGATCT	TTTATGCCTT	CTCTCCAAAT	2700
CTTGAGGTCA	CAAGTAACCT	ATCTATGGAA	ATTCGTGGAT	CTTCACGCAG	CTACAATGCA	2760
GATCTTGGAG	GTAAGTTCCA	GTTCTAA				2787

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Lys Ser Ser Leu His Trp Phe Val Ile Ser Ser Ser Leu Ala Leu
 1      5      10      15
Pro Leu Ser Leu Asn Phe Ser Ala Phe Ala Ala Val Val Glu Ile Asn
      20      25      30
Leu Gly Pro Thr Asn Ser Phe Ser Gly Pro Gly Thr Tyr Thr Pro Pro
      35      40      45
Ala Gln Thr Thr Asn Ala Asp Gly Thr Ile Tyr Asn Leu Thr Gly Asp
      50      55      60
Val Ser Ile Thr Asn Ala Gly Ser Pro Thr Ala Leu Thr Ala Ser Cys
65      70      75      80
Phe Lys Glu Thr Thr Gly Asn Leu Ser Phe Gln Gly His Gly Tyr Gln
      85      90      95
Phe Leu Leu Gln Asn Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn
      100      105      110
Thr Ala Ala Asn Lys Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser
      115      120      125
Leu Ile Gln Thr Thr Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser
      130      135      140
Thr Gly Ala Cys Ser Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln
145      150      155      160
Asn Phe Ser Asn Asp Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser
      165      170      175
Leu Ser Leu Asn Pro Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln
      180      185      190
Lys Gly Gly Ala Leu Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr
      195      200      205
Leu Asn Ser Ala Ser Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly
      210      215      220
Ala Ile Tyr Thr Glu Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile
225      230      235      240
Ser Phe Ile Asn Asn Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala
      245      250      255
Ile Tyr Cys Ser Ser Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser
      260      265      270
Asp Asn Gly Glu Leu Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly
      275      280      285
Gly Ala Ile Tyr Thr Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr
      290      295      300
Leu Phe Lys Asn Asn Ser Ala Ile Asp Thr Ala Ala Pro Leu Gly Gly
305      310      315      320
Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly
      325      330      335
Gly Asp Ile Thr Phe Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser
      340      345      350
Ser Gln Thr Thr Thr Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala
      355      360      365
Lys Ile Val Gln Leu Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr
      370      375      380
Asp Pro Ile Thr Thr Asn His Thr Ala Ala Leu Ser Asp Ala Leu Asn
385      390      395      400
Leu Asn Gly Pro Asp Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile
      405      410      415
Val Phe Ser Gly Glu Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp
      420      425      430
Asn Leu Lys Ser Thr Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln

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435	440	445
Leu Ser Leu Lys Ser Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln		
450	455	460
Ser Pro Gly Ser Thr Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr		
465	470	475
Ala Asp Gly Ile Thr Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu		480
	485	490
Lys Glu Thr Lys Lys Ala Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr		495
	500	505
Val Thr Leu Ser Gly Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val		510
	515	520
Tyr Glu Asp Val Ser Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr		525
	530	535
Leu Thr Ala Asp Asp Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala		540
545	550	555
Asp Pro Leu Glu Lys Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp		560
	565	570
Ala Leu Ser Trp Gln Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr		575
	580	585
Leu Thr Trp Thr Lys Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly		590
	595	600
Thr Leu Val Ala Asn Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser		605
	610	615
Ile Gln Gln Leu Val Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg		620
625	630	635
Gly Ile Trp Cys Glu Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr		640
	645	650
Lys Ile Asn Lys Gly Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly		655
	660	665
Ala Thr Thr Thr Leu Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys		670
	675	680
Gln Leu Phe Gly Lys Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala		685
	690	695
Ser Ala Tyr Ala Ala Ser Leu His Leu Gln His Leu Ala Thr Leu Ser		700
705	710	715
Ser Pro Ser Leu Leu Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro		720
	725	730
Val Leu Phe Asp Ala Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met		735
	740	745
Lys Thr Tyr Thr Thr Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn		750
	755	760
Asp Gly Cys Ala Leu Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu		765
	770	775
Ser His Glu Gly Leu Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu		780
785	790	795
Ala Ser Tyr Ile His Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu		800
	805	810
Val Arg Ser Phe Asp Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile		815
	820	825
Gly Ile Thr Phe Glu Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu		830
	835	840
Ala Thr Val Ile Tyr Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys		845
	850	855
Thr Thr Ala Leu Leu Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr		860
865	870	875
Asn Leu Ser Arg Gln Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala		880
	885	890
		895

Phe Ser Pro Asn Leu Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg
 900 905 910
 Gly Ser Ser Arg Ser Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2793 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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ATGAAAATAC CCTTGCACAA ACTCCTGATC TCTTCGACTC TTGTCACTCC CATTCTATTG      60
AGCATTGCAA CTTACGGAGC AGATGCTTCT TTATCCCCTA CAGATAGCTT TGATGGAGCG      120
GGCGGCTCTA CATTTACTCC AAAATCTACA GCAGATGCCA ATGGAACGAA CTATGTCTTA      180
TCAGGAAATG TCTATATAAA CGATGCTGGG AAAGGCACAG CATTAACAGG CTGCTGCTTT      240
ACAGAAACTA CGGGTGATCT GACATTTACT GGAAAGGGAT ACTCATTTTC ATTCAACACG      300
GTAGATGCGG GTTCGAATGC AGGAGCTGCG GCAAGCACAA CTGCTGATAA AGCCCTAACA      360
TTCACAGGAT TTTCTAACCT TTCCTTCATT GCAGCTCCTG GAACTACAGT TGCTTCAGGA      420
AAAAGTACTT TAAGTTCTGC AGGAGCCTTA AATCTTACCG ATAATGGAAC GATTCTCTTT      480
AGCCAAAACG TCTCCAATGA AGCTAATAAC AATGGCGGAG CGATCACCAC AAAAATCTTT      540
TCTATTTCTG GGAATACCTC TTCTATAACC TTCACTAGTA ATAGCGCAAA AAAATTAGGT      600
GGAGCGATCT ATAGCTCTGC GGCTGCAAGT ATTTCAAGGAA ACACCGGCCA GTTAGTCTTT      660
ATGAATAATA AAGGAGAAAC TGGGGGCGGG GCTCTGGGCT TTGAAGCCAG CTCCTCGATT      720
ACTCAAAATA GCTCCCTTTT CTTCTCTGGA AACACTGCAA CAGATGCTGC AGGCAAGGGC      780
GGGGCCATTT ATTGTGAAAA AACAGGAGAG ACTCCTACTC TTACTATCTC TGGAAATAAA      840
AGTCTGACCT TCGCCGAGAA CTCTTCAGTA ACTCAAGGCG GAGCAATCTG TGCCCATGGT      900
CTAGATCTTT CCGCTGCTGG CCCTACCCTA TTTTCAAATA ATAGATGCGG GAACACAGCT      960
GCAGGCAAGG GCGGCGCTAT TGCAATTGCC GACTCTGGAT CTTTAAGTCT CTCTGCAAAT     1020
CAAGGAGACA TCACGTTCTT TGGCAACACT CTAACCTCAA CCTCCGCGCC AACATCGACA     1080
CGGAATGCTA TCTACCTGGG ATCGTCAGCA AAAATTACGA ACTTAAGGGC AGCCCAAGGC     1140
CAATCTATCT ATTTCTATGA TCCGATTGCA TCTAACACCA CAGGAGCTTC AGACGTTCTG     1200
ACCATCAACC AACCGGATAG CAACTCGCCT TTAGATTATT CAGGAACGAT TGTATTTTCT     1260
GGGGAAAAGC TCTCTGCAGA TGAAGCGAAA GCTGCTGATA ACTTCACATC TATATTAAAG     1320
CAACCATTGG CTCTAGCCTC TGGAAACCTTA GCACTCAAAG GAAATGTCTG GTTAGATGTC     1380
AATGGTTTCA CACAGACTGA AGGCTCTACA CTCCTCATGC AACCAGGAAC AAAGCTCAAA     1440
GCAGATACTG AAGCTATCAG TCTTACCAAA CTTGTCTGTT ATCTTTCTGC CTTAGAGGGA     1500
AATAAGAGTG TGTCCATTGA AACAGCAGGA GCCAACAAAA CTATAACTCT AACCTCTCCT     1560
CTTGTTTTCC AAGATAGTAG CGGCAATTTT TATGAAAGCC ATACGATAAA CCAAGCCTTC     1620
ACGCAGCCTT TGGTGGTATT CACTGCTGCT ACTGCTGCTA GCGATATTTA TATCGATGCG     1680
CTTCTCACTT CTCCAGTACA AACTCCAGAA CCTCATTACG GGTATCAGGG ACATTGGGAA     1740
GCCACTTGGG CAGACACATC AACTGCAAAA TCAGGAACTA TGACTTGGGT AACTACGGGC     1800
TACAACCCTA ATCCTGAGCG TAGAGCTTCC GTAGTTCCCG ATTCATTATG GGCATCCTTT     1860
ACTGACATTC GCACTCTACA GCAGATCATG ACATCTCAAG CGAATAGTAT CTATCAGCAA     1920
CGAGGACTCT GGGCATCAGG AACTGCGAAT TTCTTCCATA AGGATAAATC AGGAACTAAC     1980
CAAGCATTCC GACATAAAAG CTACGGCTAT ATTGTTGGAG GAAGTGCTGA AGATTTTCTCT     2040
GAAAATATCT TCAGTGATAG TTTCTGCCAG CTCTTCGGTA AAGATAAAGA CCTGTTTATA     2100
GTTGAAAATA CCTCTATAA CTATTTAGCG TCGCTATACC TGCAACATCG AGCATTCTTA     2160
GGAGGACTTC CCATGCCCTC ATTTGGAAGT ATCACCGACA TGCTGAAAGA TATTCCTCTC     2220
ATTTTGAATG CCCAGCTAAG CTACAGCTAC ACTAAAAATG ATATGGATAC TCGCTATACT     2280
TCCTATCTCG AAGCTCAAGG TTCTTGACC AATAATTCTG GGGCTCTAGA GCTCGGAGGA     2340
TCTCTGGCTC TATATCTCCC TAAAGAAGCA CCGTTCTTCC AGGGATATTT CCCCTTCTTA     2400

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AAGTTCCAGG	CAGTCTACAG	CCGCCAACAA	AACTTTAAAG	AGAGTGGCGC	TGAAGCCCGT	2460
GCTTTTGATG	ATGGAGACCT	AGTGAAGTGC	TCTATCCCTG	TCGGCATTCTG	GTTAGAAAAA	2520
ATCTCCGAAG	ATGAAAAAAA	TAATTTTCGAG	ATTTCTCTAG	CCAACATTGG	TGATGTGTAT	2580
CGTAAAAATC	CCCGTTCGCG	TACTTCTCTA	ATGCTCAGTG	GAGCCTCTTG	GACTTCGCTA	2640
TGTAAAAACC	TCGCACGACA	AGCCTTCTTA	GCAAGTGCTG	GAAGCCATCT	GACTCTCTCC	2700
CCTCATGTAG	AACTCTCTGG	GGAAGCTGCT	TATGAGCTTC	GTGGCTCAGC	ACACATCTAC	2760
AATGTAGATT	GTGGGCTAAG	ATACTCATTC	TAG			2793

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Lys	Ile	Pro	Leu	His	Lys	Leu	Leu	Ile	Ser	Ser	Thr	Leu	Val	Thr
1				5					10					15	
Pro	Ile	Leu	Leu	Ser	Ile	Ala	Thr	Tyr	Gly	Ala	Asp	Ala	Ser	Leu	Ser
			20					25					30		
Pro	Thr	Asp	Ser	Phe	Asp	Gly	Ala	Gly	Gly	Ser	Thr	Phe	Thr	Pro	Lys
		35					40					45			
Ser	Thr	Ala	Asp	Ala	Asn	Gly	Thr	Asn	Tyr	Val	Leu	Ser	Gly	Asn	Val
		50				55					60				
Tyr	Ile	Asn	Asp	Ala	Gly	Lys	Gly	Thr	Ala	Leu	Thr	Gly	Cys	Cys	Phe
65					70				75						80
Thr	Glu	Thr	Thr	Gly	Asp	Leu	Thr	Phe	Thr	Gly	Lys	Gly	Tyr	Ser	Phe
				85				90						95	
Ser	Phe	Asn	Thr	Val	Asp	Ala	Gly	Ser	Asn	Ala	Gly	Ala	Ala	Ala	Ser
			100					105						110	
Thr	Thr	Ala	Asp	Lys	Ala	Leu	Thr	Phe	Thr	Gly	Phe	Ser	Asn	Leu	Ser
		115				120					125				
Phe	Ile	Ala	Ala	Pro	Gly	Thr	Thr	Val	Ala	Ser	Gly	Lys	Ser	Thr	Leu
		130				135					140				
Ser	Ser	Ala	Gly	Ala	Leu	Asn	Leu	Thr	Asp	Asn	Gly	Thr	Ile	Leu	Phe
145					150					155					160
Ser	Gln	Asn	Val	Ser	Asn	Glu	Ala	Asn	Asn	Asn	Gly	Gly	Ala	Ile	Thr
			165					170						175	
Thr	Lys	Thr	Leu	Ser	Ile	Ser	Gly	Asn	Thr	Ser	Ser	Ile	Thr	Phe	Thr
			180					185					190		
Ser	Asn	Ser	Ala	Lys	Lys	Leu	Gly	Gly	Ala	Ile	Tyr	Ser	Ser	Ala	Ala
		195					200					205			
Ala	Ser	Ile	Ser	Gly	Asn	Thr	Gly	Gln	Leu	Val	Phe	Met	Asn	Asn	Lys
		210				215					220				
Gly	Glu	Thr	Gly	Gly	Gly	Ala	Leu	Gly	Phe	Glu	Ala	Ser	Ser	Ser	Ile
225					230					235					240
Thr	Gln	Asn	Ser	Ser	Leu	Phe	Phe	Ser	Gly	Asn	Thr	Ala	Thr	Asp	Ala
			245						250					255	
Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Cys	Glu	Lys	Thr	Gly	Glu	Thr	Pro
			260					265					270		
Thr	Leu	Thr	Ile	Ser	Gly	Asn	Lys	Ser	Leu	Thr	Phe	Ala	Glu	Asn	Ser
		275				280						285			
Ser	Val	Thr	Gln	Gly	Gly	Ala	Ile	Cys	Ala	His	Gly	Leu	Asp	Leu	Ser

290	295	300
Ala Ala Gly Pro Thr Leu	Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala	
305	310	315
Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser		320
	325	330
Leu Ser Ala Asn Gln Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr		335
	340	345
Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser		350
	355	360
Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr		365
	370	375
Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu		380
385	390	395
Thr Ile Asn Gln Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr		400
	405	410
Ile Val Phe Ser Gly Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala		415
	420	425
Asp Asn Phe Thr Ser Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly		430
	435	440
Thr Leu Ala Leu Lys Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr		445
	450	455
Gln Thr Glu Gly Ser Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys		460
465	470	475
Ala Asp Thr Glu Ala Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser		480
	485	490
Ala Leu Glu Gly Asn Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn		495
	500	505
Lys Thr Ile Thr Leu Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly		510
	515	520
Asn Phe Tyr Glu Ser His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu		525
	530	535
Val Val Phe Thr Ala Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala		540
545	550	555
Leu Leu Thr Ser Pro Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln		560
	565	570
Gly His Trp Glu Ala Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly		575
	580	585
Thr Met Thr Trp Val Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg		590
	595	600
Ala Ser Val Val Pro Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg		605
	610	615
Thr Leu Gln Gln Ile Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln		620
625	630	635
Arg Gly Leu Trp Ala Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys		640
	645	650
Ser Gly Thr Asn Gln Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val		655
	660	665
Gly Gly Ser Ala Glu Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe		670
	675	680
Cys Gln Leu Phe Gly Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr		685
	690	695
Ser His Asn Tyr Leu Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu		700
705	710	715
Gly Gly Leu Pro Met Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys		720
	725	730
Asp Ile Pro Leu Ile Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys		735
	740	745
		750

Asn Asp Met Asp Thr Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser
 755 760 765
 Trp Thr Asn Asn Ser Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu
 770 775 780
 Tyr Leu Pro Lys Glu Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu
 785 790 795 800
 Lys Phe Gln Ala Val Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly
 805 810 815
 Ala Glu Ala Arg Ala Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile
 820 825 830
 Pro Val Gly Ile Arg Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn
 835 840 845
 Phe Glu Ile Ser Leu Ala Asn Ile Gly Asp Val Tyr Arg Lys Asn Pro
 850 855 860
 Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu
 865 870 875 880
 Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His
 885 890 895
 Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu
 900 905 910
 Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr
 915 920 925
 Ser Phe
 930

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAAGACAATA	TAAGGTACCG	TCATAACAGC	GGGGGTTATG	CACTAGGGAT	CACAGCAACA	60
ACTCCTGCCG	AGGATCAGCT	TACTTTTGCC	TTCTGCCAGC	TCCTTGCTAG	AGATCGCAAT	120
CATATTACAG	GTAAGAACCA	CGGAGATACT	TACGGTGCCT	CTTTGTATTT	CCACCATACA	180
GAAGGGCTCT	TCGACATCGC	CAATTTCTCT	TGGGGAAAAG	CAACCCGAGC	TCCCTGGGTG	240
CTCTCTGAGA	TCTCCCAGAT	CATTCCTTTA	TCGTTCGATG	CTAAATTCAG	TTATCTCCAT	300
ACAGACAACC	ACATGAAGAC	ATATTATACC	GATAACTCTA	TCATCAAGGG	TTCTTGGAGA	360
AACGATGCCT	TCTGTGCAGA	TCTTGGAGCT	AGCCTGCCTT	TTGTTATTTT	CGTTCCGTAT	420
CTTCTGAAAG	AAGTCGAACC	TTTTGTCAAA	GTACAGTATA	TCTATGCGCA	TCAGCAAGAC	480
TTCTACGAGC	GTCATGCTGA	AGGACGCGCT	TTCAATAAAA	GCGAGCTTAT	CAACGTAGAG	540
ATTCTATAG	GCGTCACCTT	CGAAAGAGAC	TCAAAATCAG	AAAAGGGAAC	TTACGATCTT	600
ACTCTTATGT	ATATACTCGA	TGCTTACCGA	CGCAATCCTA	AATGTCAAAC	TTCCCTAATA	660
GCTAGCGATG	CTAACTGGAT	GGCCTATGGT	ACCAACCTCG	CACGACAAGG	TTTTTCGTGT	720
CGTGCTGCGA	ACCATTTCCA	AGTGAACCCC	CACATGGAAA	TCTTCGGTCA	ATTCGCTTTT	780
GAAGTACGAA	GTTCTTCACG	AAATTATAAT	ACAAACCTAG	GCTCTAAGTT	TTGTTTCTAG	840

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Ala Leu Gly
 1           5           10           15
Ile Thr Ala Thr Thr Pro Ala Glu Asp Gln Leu Thr Phe Ala Phe Cys
          20           25           30
Gln Leu Phe Ala Arg Asp Arg Asn His Ile Thr Gly Lys Asn His Gly
          35           40           45
Asp Thr Tyr Gly Ala Ser Leu Tyr Phe His His Thr Glu Gly Leu Phe
          50           55           60
Asp Ile Ala Asn Phe Leu Trp Gly Lys Ala Thr Arg Ala Pro Trp Val
65           70           75           80
Leu Ser Glu Ile Ser Gln Ile Ile Pro Leu Ser Phe Asp Ala Lys Phe
          85           90           95
Ser Tyr Leu His Thr Asp Asn His Met Lys Thr Tyr Tyr Thr Asp Asn
          100          105          110
Ser Ile Ile Lys Gly Ser Trp Arg Asn Asp Ala Phe Cys Ala Asp Leu
          115          120          125
Gly Ala Ser Leu Pro Phe Val Ile Ser Val Pro Tyr Leu Leu Lys Glu
          130          135          140
Val Glu Pro Phe Val Lys Val Gln Tyr Ile Tyr Ala His Gln Gln Asp
145          150          155          160
Phe Tyr Glu Arg His Ala Glu Gly Arg Ala Phe Asn Lys Ser Glu Leu
          165          170          175
Ile Asn Val Glu Ile Pro Ile Gly Val Thr Phe Glu Arg Asp Ser Lys
          180          185          190
Ser Glu Lys Gly Thr Tyr Asp Leu Thr Leu Met Tyr Ile Leu Asp Ala
          195          200          205
Tyr Arg Arg Asn Pro Lys Cys Gln Thr Ser Leu Ile Ala Ser Asp Ala
          210          215          220
Asn Trp Met Ala Tyr Gly Thr Asn Leu Ala Arg Gln Gly Phe Ser Val
225          230          235          240
Arg Ala Ala Asn His Phe Gln Val Asn Pro His Met Glu Ile Phe Gly
          245          250          255
Gln Phe Ala Phe Glu Val Arg Ser Ser Ser Arg Asn Tyr Asn Thr Asn
          260          265          270
Leu Gly Ser Lys Phe Cys Phe
          275

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGACCATAC TTCGAAATTT TCTTACCTGC TCGGCTTTAT TCCTCGCTCT CCCTGCAGCA

60

GCACAAGTTG	TATATCTTCA	TGAAAGTGAT	GGTTATAACG	GTGCTATCAA	TAATAAAAGC	120
TTAGAACCTA	AAATTACCTG	TTATCCAGAA	GGAACCTTCT	ACATCTTTCT	AGATGACGTG	180
AGGATTTCCA	ACGTTAAGCA	TGATCAAGAA	GATGCTGGGG	TTTTTATAAA	TCGATCTGGG	240
AATCTTTTTT	TCATGGGCAA	CCGTTGCAAC	TTCACTTTTT	ACAACCTTAT	GACCGAGGGT	300
TTTGGCGCTG	CCATTTTCGAA	CCGCGTTGGA	GACACCACTC	TCACTCTCTC	TAATTTTTTCT	360
TACTTAACGT	TCACCTCAGC	ACCTCTACTA	CCTCAAGGAC	AAGGAGCGAT	TTATAGTCTT	420
GGTTCCTGTA	TGATCGAAAA	TAGTGAGGAA	GTGACTTTCT	GTGGGAACTA	CTCTTCGTGG	480
AGTGAGAGCTG	CGATTTATAC	TCCCTACCTT	TTAGGTTCTA	AGGCGAGTCG	TCCTTCAGTA	540
AATCTCAGCG	GGAACCGCTA	CCTGGTGTTT	AGAGACTATG	TGAGCCAAGG	TTATGGCGGC	600
GCCGTATCTA	CCCACAATCT	CACACTCACG	ACTCGAGGAC	CTTCGTGTTT	TGAAAATAAT	660
CATGCTTATC	ATGACGTGAA	TAGTAATGGA	GGAGCCATTG	CCATTGCTCC	TGGAGGATCG	720
ATCTCTATAT	CCGTGAAAAG	CGGAGATCTC	ATCTTCAAAG	GAAATACAGC	ATCACAAGAC	780
GGAAATACAA	TACACAATC	CATCCATCTG	CAATCTGGAG	CACAGTTTAA	GAACCTACGT	840
GCTGTTTCAG	AATCCGGAGT	TTATTTCTAT	GATCCTATAA	GCCATAGCGA	GTCGCATAAA	900
ATTACAGATC	TTGTAATCAA	TGCTCCTGAA	GGAAAGGAAA	CTTATGAAGG	AACAATTAGC	960
TTCTCAGGAC	TATGCCTGGA	TGATCATGAA	GTTTGTGCGG	AAAATCTTAC	TTCCACAATC	1020
CTACAAGATG	TCACATTAGC	AGGAGGAACT	CTCTCTCTAT	CGGATGGGGT	TACCTTGCAA	1080
CTGCATTCTT	TTAAGCAGGA	AGCAAGCTCT	ACGCTTACTA	TGTCTCCAGG	AACCACTCTG	1140
CTCTGCTCAG	GAGATGCTCG	GGTTCAGAAT	CTGCACATCC	TGATTGAAGA	TACCGACAAC	1200
TTTGTTCCCTG	TAAGGATTCG	CGCCGAGGAC	AAGGATGCTC	TTGTCTCATT	AGAAAACTT	1260
AAAGTTGCCT	TTGAGGCTTA	TTGGTCCGTC	TATGACTTTC	CTCAATTTAA	GGAAGCCTTT	1320
ACGATTCCTC	TTCTTGAAT	TCTAGGGCCT	TCTTTTGACA	GTCTTCTCCT	AGGGGAGACC	1380
ACTTTGGAGA	GAACCCAAGT	CACAACAGAG	AATGACGCCG	TTGAGGTTT	CTGGTCCCTA	1440
AGCTGGGAAG	AGTACCCCCC	TTCTCTGGAT	AAAGACAGAA	GGATCACACC	AACTAAGAAA	1500
ACTGTTTTCC	TCACTTGGA	TCCTGAGATC	ACTTCTACGC	CATAA		1545

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Thr	Ile	Leu	Arg	Asn	Phe	Leu	Thr	Cys	Ser	Ala	Leu	Phe	Leu	Ala
1				5					10					15	
Leu	Pro	Ala	Ala	Ala	Gln	Val	Val	Tyr	Leu	His	Glu	Ser	Asp	Gly	Tyr
			20					25					30		
Asn	Gly	Ala	Ile	Asn	Asn	Lys	Ser	Leu	Glu	Pro	Lys	Ile	Thr	Cys	Tyr
		35				40					45				
Pro	Glu	Gly	Thr	Ser	Tyr	Ile	Phe	Leu	Asp	Asp	Val	Arg	Ile	Ser	Asn
	50					55					60				
Val	Lys	His	Asp	Gln	Glu	Asp	Ala	Gly	Val	Phe	Ile	Asn	Arg	Ser	Gly
65				70					75					80	
Asn	Leu	Phe	Phe	Met	Gly	Asn	Arg	Cys	Asn	Phe	Thr	Phe	His	Asn	Leu
			85					90						95	
Met	Thr	Glu	Gly	Phe	Gly	Ala	Ala	Ile	Ser	Asn	Arg	Val	Gly	Asp	Thr
		100						105					110		
Thr	Leu	Thr	Leu	Ser	Asn	Phe	Ser	Tyr	Leu	Thr	Phe	Thr	Ser	Ala	Pro
	115					120					125				
Leu	Leu	Pro	Gln	Gly	Gln	Gly	Ala	Ile	Tyr	Ser	Leu	Gly	Ser	Val	Met
	130					135					140				
Ile	Glu	Asn	Ser	Glu	Glu	Val	Thr	Phe	Cys	Gly	Asn	Tyr	Ser	Ser	Trp

145		150		155		160
Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser						
	165		170		175	
Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp						
	180		185		190	
Tyr Val Ser Gln Gly Tyr Gly Gly Ala Val Ser Thr His Asn Leu Thr						
	195		200		205	
Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His						
	210		215		220	
Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser						
225	230		235		240	
Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr						
	245		250		255	
Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser						
	260		265		270	
Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr						
	275		280		285	
Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu						
	290		295		300	
Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser						
305	310		315		320	
Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu						
	325		330		335	
Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser						
	340		345		350	
Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala						
	355		360		365	
Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly						
	370		375		380	
Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn						
385	390		395		400	
Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser						
	405		410		415	
Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp						
	420		425		430	
Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu						
	435		440		445	
Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg						
	450		455		460	
Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu						
465	470		475		480	
Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr						
	485		490		495	
Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser						
	500		505		510	
Thr Pro						

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAAAACGT	CTATTCGTAA	GTTCTTAATT	TCTACCACAC	TGGCGCCATG	TTTTGCTTCA	60
ACAGCGTTTA	CTGTAGAAGT	TATCATGCCT	TCCGAGAACT	TTGATGGATC	GAGTGGGAAG	120
ATTTTTCCTT	ACACAACACT	TTCTGATCCT	AGAGGGACAC	TCTGTATTTT	TTCAGGGGAT	180
CTCTACATTG	CGAATCTTGA	TAATGCCATA	TCCAGAACCT	CTTCCAGTTG	CTTTAGCAAT	240
AGGGCGGGAG	CACTACAAAT	CTTAGGAAAA	GGTGGGGTTT	TCTCCTTCTT	AAATATCCGT	300
TCTTCAGCTG	ACGGAGCCGC	GATTAGTAGT	GTAATCACCC	AAAATCCTGA	ACTATGTCCC	360
TTGAGTTTTT	CAGGATTTAG	TCAGATGATC	TTCGATAACT	GTGAATCTTT	GACTTCAGAT	420
ACCTCAGCGA	GTAATGTCAT	ACCTCACGCA	TCGGCGATTT	ACGCTACAAC	GCCCATGCTC	480
TTTACAAACA	ATGACTCCAT	ACTATTCCAA	TACAACCGTT	CTGCAGGATT	TGGAGCTGCC	540
ATTTCGAGGCA	CAAGCATCAC	AATAGAAAAT	ACGAAAAAGA	GCCTTCTCTT	TAATGGTAAT	600
GGATCCATCT	CTAATGGAGG	GGCCCTCACG	GGATCTGCAG	CGATCAACCT	CATCAACAAT	660
AGCGCTCCTG	TGATTTTCTC	AACGAATGCT	ACAGGGATCT	ATGGTGGGGC	TATTTACCTT	720
ACCGGAGGAT	CTATGCTCAC	CTCTGGGAAC	CTCTCAGGAG	TCTTGTTTCG	TTATAATAGC	780
TCGCGCT						787

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Lys	Thr	Ser	Ile	Arg	Lys	Phe	Leu	Ile	Ser	Thr	Thr	Leu	Ala	Pro
1				5				10						15	
Cys	Phe	Ala	Ser	Thr	Ala	Phe	Thr	Val	Glu	Val	Ile	Met	Pro	Ser	Glu
			20					25					30		
Asn	Phe	Asp	Gly	Ser	Ser	Gly	Lys	Ile	Phe	Pro	Tyr	Thr	Thr	Leu	Ser
		35					40					45			
Asp	Pro	Arg	Gly	Thr	Leu	Cys	Ile	Phe	Ser	Gly	Asp	Leu	Tyr	Ile	Ala
	50					55					60				
Asn	Leu	Asp	Asn	Ala	Ile	Ser	Arg	Thr	Ser	Ser	Ser	Cys	Phe	Ser	Asn
65					70					75					80
Arg	Ala	Gly	Ala	Leu	Gln	Ile	Leu	Gly	Lys	Gly	Gly	Val	Phe	Ser	Phe
				85				90						95	
Leu	Asn	Ile	Arg	Ser	Ser	Ala	Asp	Gly	Ala	Ala	Ile	Ser	Ser	Val	Ile
			100					105						110	
Thr	Gln	Asn	Pro	Glu	Leu	Cys	Pro	Leu	Ser	Phe	Ser	Gly	Phe	Ser	Gln
		115					120					125			
Met	Ile	Phe	Asp	Asn	Cys	Glu	Ser	Leu	Thr	Ser	Asp	Thr	Ser	Ala	Ser
	130					135					140				
Asn	Val	Ile	Pro	His	Ala	Ser	Ala	Ile	Tyr	Ala	Thr	Thr	Pro	Met	Leu
145					150					155					160
Phe	Thr	Asn	Asn	Asp	Ser	Ile	Leu	Phe	Gln	Tyr	Asn	Arg	Ser	Ala	Gly
				165					170					175	
Phe	Gly	Ala	Ala	Ile	Arg	Gly	Thr	Ser	Ile	Thr	Ile	Glu	Asn	Thr	Lys
			180				185					190			
Lys	Ser	Leu	Leu	Phe	Asn	Gly	Asn	Gly	Ser	Ile	Ser	Asn	Gly	Gly	Ala
		195					200					205			
Leu	Thr	Gly	Ser	Ala	Ala	Ile	Asn	Leu	Ile	Asn	Asn	Ser	Ala	Pro	Val
	210					215					220				

Ile Phe Ser Thr Asn Ala Thr Gly Ile Tyr Gly Gly Ala Ile Tyr Leu
 225 230 235 240
 Thr Gly Gly Ser Met Leu Thr Ser Gly Asn Leu Ser Gly Val Leu Phe
 245 250 255
 Val Tyr Asn Ser Ser Arg
 260

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2838 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAAGACTT	CAGTTTCTAT	GTTGTTGGCC	CTGCTTTGCT	CGGGGGCTAG	CTCTATTGTA	60
CTCCATGCCG	CAACCACTCC	ACTAAATCCT	GAAGATGGGT	TTATTGGGGA	GGGCAATACA	120
AATACTTTT	CTCCGAAATC	TACAACGGAT	GCTGCAGGAA	CTACCTACTC	TCTCACAGGA	180
GAGGTTCTGT	TTATAGATCC	GGGGAAAGGT	GTTCAATTA	CAGGAACTTG	CTTTGTAGAA	240
ACTGCTGGCG	ATCTTACATT	TTTAGGTAAT	GGAAATACCC	TAAAGTTCCT	GTCGGTAGAT	300
GCAGGTGCTA	ATATCGCGGT	TGCTCATGTA	CAAGGAAGTA	AGAATTTAAG	CTTCACAGAT	360
TTCCTTTCTC	TGGTGATCAC	AGAATCTCCA	AAATCCGCTG	TTAGTACAGG	AAAAGGTAGC	420
CTAGTCAGTT	CAGGTGCAGT	CCAAC TGCAA	GATATAAACA	CTCTAGTTCT	TACAAGCAAT	480
GCCTCTGTCT	AAGATGGTGG	CGTGATTAAA	GGAACTCCT	GCTTGATTCA	GGGAATCAAA	540
AATAGTGCGA	TTTTTGGACA	AAATACATCT	TCGAAAAAAG	GAGGGGCGAT	CTCCACGACT	600
CAAGGACTCA	CCATAGAGAA	TAACTTAGGG	ACGCTAAAGT	TCAATGAAAA	CAAAGCAGTG	660
ACCTCAGGAG	GCGCCTTAGA	TTTAGGAGCC	GCGTCTACAT	TCACTGCGAA	CCATGAGTTG	720
ATATTTTCAC	AAAATAAGAC	TTCTGGGAAT	GCTGCAAATG	GCGGAGCCAT	AAATTGCTCA	780
GGCGACCTAA	CATTTACTGA	TAACACTTCT	TTGTTACTTC	AAGAAAATAG	CACAATGCAG	840
GATGGTGGAG	CTTTGTGTAG	CACAGGAACC	ATAAGCATT	CCGGTAGTGA	TTCTATCAAT	900
GTGATAGGAA	ATACTTCAGG	ACAAAAAGGA	GGAGCGATT	CTGCAGCTTC	TCTCAAGATT	960
TTGGGAGGGC	AGGGAGGCGC	TCTCTTTTCT	AATAACGTAG	TGACTCATGC	CACCCCTCTA	1020
GGAGGTGCCA	TTTTTATCAA	CACAGGAGGA	TCCTTGACGC	TCTTCACTCA	AGGAGGGGAT	1080
ATCGTATTTC	AGGGGAATCA	GGTCACTACA	ACAGCTCCAA	ATGCTACCAC	TAAGAGAAAT	1140
GTAATTCACC	TCGAGAGCAC	CGCGAAGTGG	ACGGGACTTG	CTGCAAGTCA	AGGTAACGCT	1200
ATCTATTTCT	ATGATCCCAT	TACCACCAAC	GATACGGGAG	CAAGCGATAA	CTTACGTATC	1260
AATGAGGTCA	GTGCAAATCA	AAAGCTCTCG	GGATCTATAG	TATTTTCTGG	AGAGAGATTG	1320
TCGACAGCAG	AAGCTATAGC	TGAAAATCTT	ACTTCGAGGA	TCAACCAGCC	TGTCACTTTA	1380
GTAGAGGGGA	GCTTAGAACT	TAAACAGGGA	GTGACCTTGA	TCACACAAGG	ATTCTCGCAG	1440
GAGCCAGAAT	CCACGCTTCT	TTTGGATTGT	GGGACCTCAT	TACAAGCTTC	TACAGAAGAT	1500
ATCGTCATCA	CAAATTCATC	TATAAATGCC	GATACCATT	ACGGAAAGAA	TCCAATCAAT	1560
ATTGTAGCTT	CAGCAGCGAA	TAAGAACATT	ACCCTAACAG	GAACCTTAGC	ACTTGTAAT	1620
GCAGATGGAG	CTTTGTATGA	GAACCATACC	TTGCAAGACT	CTCAAGATTA	TAGCTTTGTA	1680
AAGTTATCTC	CAGGAGCGGG	AGGGACTATA	ATTACTCAAG	ATGCTTCTCA	GAAGCTTCTT	1740
GAAGTAGCTC	CTTCTAGACC	ACATTATGGC	TATCAAGGAC	ATTGGAATGT	GCAAGTCATC	1800
CCAGGAACGG	GAAC TCAACC	GAGCCAGGCA	AATTTAGAAT	GGGTGCGGAC	AGGATACCTT	1860
CCGAATCCCG	AACGGCAAGG	ATTTT TAGTT	CCCAATAGCC	TGTGGGGTTC	TTTTGTTGAT	1920
CAGCGTGCTA	TCCAAGAAAT	CATGGTAAAT	AGTAGCCAAA	TCTTATGTCA	GGAACGGGGA	1980
GTCTGGGGAG	CTGGAATTGC	TAATTTCCCTA	CATAGAGATA	AAATTAATGA	GCACGGCTAT	2040
CGCCATAGCG	GTGTCGGTTA	TCTTGTGGGA	GTTGGGACTC	ATGCTTTTTC	TGATGCTACG	2100
ATAAATGCGG	CTTTT TGCCA	GCTCTTCAGT	AGAGATAAAG	ACTACGTAGT	ATCCAAAAAT	2160
CATGGAAC TA	GCTACTCAGG	GGTCGTATTT	CTTGAGGATA	CCCTAGAGTT	TAGAAGTCCA	2220
CAGGGATTCT	ATACTGATAG	CTCCTCAGAA	GCTTGCTGTA	ACCAAGTCGT	CACTATAGAT	2280

ATGCAGTTGT	CTTACAGCCA	TAGAAATAAT	GATATGAAAA	CCAAATACAC	GACATATCCA	2340
GAAGCTCAGG	GATCTTGGGC	AAATGATGTT	TTTGGTCTTG	AGTTTGGAGC	GACTACATAC	2400
TACTACCCTA	ACAGTACTTT	TTTATTTGAT	TACTACTCTC	CGTTTCTCAG	GCTGCAGTGC	2460
ACCTATGCTC	ACCAGGAAGA	CTTCAAAGAG	ACAGGAGGTG	AGGTTCGTCA	CTTTACTAGC	2520
GGAGATCTTT	TCAATTTAGC	AGTTCCTATT	GGCGTGAAGT	TTGAGAGATT	TTCAGACTGT	2580
AAAAGGGGAT	CTTATGAACT	TACCCTTGCT	TATGTTCTTG	ATGTGATTCTG	CAAAGATCCC	2640
AAGAGCACGG	CAACATTGGC	TAGTGGAGCT	ACGTGGAGCA	CCCACGGAAA	CAATCTCTCC	2700
AGACAAGGAT	TACAACTGCG	TTTAGGGAAC	CACTGTCTCA	TAAATCCTGG	AATTGAGGTG	2760
TTCACTCACG	GAGCTATTGA	ATTGCGGGGA	TCCTCTCGTA	ATTATAACAT	CAATCTCGGG	2820
GGTAAATACC	GATTTTAA					2838

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Lys	Thr	Ser	Val	Ser	Met	Leu	Leu	Ala	Leu	Leu	Cys	Ser	Gly	Ala
1				5					10					15	
Ser	Ser	Ile	Val	Leu	His	Ala	Ala	Thr	Pro	Leu	Asn	Pro	Glu	Asp	
			20					25				30			
Gly	Phe	Ile	Gly	Glu	Gly	Asn	Thr	Asn	Thr	Phe	Ser	Pro	Lys	Ser	Thr
	35					40				45					
Thr	Asp	Ala	Ala	Gly	Thr	Thr	Tyr	Ser	Leu	Thr	Gly	Glu	Val	Leu	Phe
	50					55				60					
Ile	Asp	Pro	Gly	Lys	Gly	Gly	Ser	Ile	Thr	Gly	Thr	Cys	Phe	Val	Glu
65				70					75					80	
Thr	Ala	Gly	Asp	Leu	Thr	Phe	Leu	Gly	Asn	Gly	Asn	Thr	Leu	Lys	Phe
			85					90					95		
Leu	Ser	Val	Asp	Ala	Gly	Ala	Asn	Ile	Ala	Val	Ala	His	Val	Gln	Gly
		100					105					110			
Ser	Lys	Asn	Leu	Ser	Phe	Thr	Asp	Phe	Leu	Ser	Leu	Val	Ile	Thr	Glu
	115					120					125				
Ser	Pro	Lys	Ser	Ala	Val	Ser	Thr	Gly	Lys	Gly	Ser	Leu	Val	Ser	Ser
	130					135					140				
Gly	Ala	Val	Gln	Leu	Gln	Asp	Ile	Asn	Thr	Leu	Val	Leu	Thr	Ser	Asn
145				150					155					160	
Ala	Ser	Val	Glu	Asp	Gly	Gly	Val	Ile	Lys	Gly	Asn	Ser	Cys	Leu	Ile
			165					170					175		
Gln	Gly	Ile	Lys	Asn	Ser	Ala	Ile	Phe	Gly	Gln	Asn	Thr	Ser	Ser	Lys
		180					185					190			
Lys	Gly	Gly	Ala	Ile	Ser	Thr	Thr	Gln	Gly	Leu	Thr	Ile	Glu	Asn	Asn
	195					200					205				
Leu	Gly	Thr	Leu	Lys	Phe	Asn	Glu	Asn	Lys	Ala	Val	Thr	Ser	Gly	Gly
	210					215				220					
Ala	Leu	Asp	Leu	Gly	Ala	Ala	Ser	Thr	Phe	Thr	Ala	Asn	His	Glu	Leu
225				230					235					240	
Ile	Phe	Ser	Gln	Asn	Lys	Thr	Ser	Gly	Asn	Ala	Ala	Asn	Gly	Gly	Ala
			245					250					255		
Ile	Asn	Cys	Ser	Gly	Asp	Leu	Thr	Phe	Thr	Asp	Asn	Thr	Ser	Leu	Leu
		260					265					270			

Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr
 275 280 285
 Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn
 290 295 300
 Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile
 305 310 315 320
 Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
 325 330 335
 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
 340 345 350
 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
 355 360 365
 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
 370 375 380
 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
 385 390 395 400
 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
 405 410 415
 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
 420 425 430
 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
 435 440 445
 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
 450 455 460
 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
 465 470 475 480
 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala
 485 490 495
 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr
 500 505 510
 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys
 515 520 525
 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala
 530 535 540
 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val
 545 550 555 560
 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser
 565 570 575
 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln
 580 585 590
 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser
 595 600 605
 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu
 610 615 620
 Arg Gln Gly Phe Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp
 625 630 635 640
 Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu Cys
 645 650 655
 Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His Arg
 660 665 670
 Asp Lys Ile Asn Glu His Gly Tyr Arg His Ser Gly Val Gly Tyr Leu
 675 680 685
 Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala Ala
 690 695 700
 Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys Asn
 705 710 715 720
 His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu Glu

ATCAGGTGAT	AAAAGTTCCT	CGTTAGCTAG	TGACTGTAGG	TGACATGAGA	AAGCTAACAC	60
GGAGGAAACT	AAAACCCAAG	GAATCGAAGT	CTTCATGGTA	ATGCTTTTGT	TTTTTAGAGA	120
ACTATTTCGA	TCAATATAGA	AACAAAATAA	GTAAATCAAG	TTAAAGATGA	CAAAACAGCT	180
GTCAAGAATT	TTTATCTTGA	CTCTCTGAGT	TTTCTATTTT	ATATGACGCA	AGTAAGAATT	240
TAATAATAAA	GTGGGTTT	ATG AAA TCG CAA TTT TCC	TGG TTA GTG CTC TCT			291
		Met Lys Ser Gln Phe Ser	Trp Leu Val Leu Ser			
	1		5		10	

TCG	ACA	TTG	GCA	TGT	TTT	ACT	AGT	TGT	TCC	ACT	GTT	TTT	GCT	GCA	ACT	339
Ser	Thr	Leu	Ala	Cys	Phe	Thr	Ser	Cys	Ser	Thr	Val	Phe	Ala	Ala	Thr	
		15						20					25			
GCT	GAA	AAT	ATA	GGC	CCC	TCT	GAT	AGC	TTT	GAC	GGA	AGT	ACT	AAC	ACA	387
Ala	Glu	Asn	Ile	Gly	Pro	Ser	Asp	Ser	Phe	Asp	Gly	Ser	Thr	Asn	Thr	
	30						35					40				
GGC	ACC	TAT	ACT	CCT	AAA	AAT	ACG	ACT	ACT	GGA	ATA	GAC	TAT	ACT	CTG	435
Gly	Thr	Tyr	Thr	Pro	Lys	Asn	Thr	Thr	Thr	Gly	Ile	Asp	Tyr	Thr	Leu	
	45					50					55					
ACA	GGA	GAT	ATA	ACT	CTG	CAA	AAC	CTT	GGG	GAT	TCG	GCA	GCT	TTA	ACG	483
Thr	Gly	Asp	Ile	Thr	Leu	Gln	Asn	Leu	Gly	Asp	Ser	Ala	Ala	Leu	Thr	
60					65				70					75		
AAG	GGT	TGT	TTT	TCT	GAC	ACT	ACG	GAA	TCT	TTA	AGC	TTT	GCC	GGT	AAG	531
Lys	Gly	Cys	Phe	Ser	Asp	Thr	Thr	Glu	Ser	Leu	Ser	Phe	Ala	Gly	Lys	
			80					85					90			
GGG	TAC	TCA	CTT	TCT	TTT	TTA	AAT	ATT	AAG	TCT	AGT	GCT	GAA	GGC	GCA	579
Gly	Tyr	Ser	Leu	Ser	Phe	Leu	Asn	Ile	Lys	Ser	Ser	Ala	Glu	Gly	Ala	
		95					100						105			
GCA	CTT	TCT	GTT	ACA	ACT	GAT	AAA	AAT	CTG	TCG	CTA	ACA	GGA	TTT	TCG	627
Ala	Leu	Ser	Val	Thr	Thr	Asp	Lys	Asn	Leu	Ser	Leu	Thr	Gly	Phe	Ser	
	110						115					120				
AGT	CTT	ACT	TTC	TTA	GCG	GCC	CCA	TCA	TCG	GTA	ATC	ACA	ACC	CCC	TCA	675
Ser	Leu	Thr	Phe	Leu	Ala	Ala	Pro	Ser	Ser	Val	Ile	Thr	Thr	Pro	Ser	
	125					130					135					
GGA	AAA	GGT	GCA	GTT	AAA	TGT	GGA	GGG	GAT	CTT	ACA	TTT	GAT	AAC	AAT	723
Gly	Lys	Gly	Ala	Val	Lys	Cys	Gly	Gly	Asp	Leu	Thr	Phe	Asp	Asn	Asn	
140					145				150					155		
GGA	ACT	ATT	TTA	TTT	AAA	CAA	GAT	TAC	TGT	GAG	GAA	AAT	GGC	GGA	GCC	771
Gly	Thr	Ile	Leu	Phe	Lys	Gln	Asp	Tyr	Cys	Glu	Glu	Asn	Gly	Gly	Ala	
			160					165					170			
ATT	TCT	ACC	AAG	AAT	CTT	TCT	TTG	AAA	AAC	AGC	ACG	GGA	TCG	ATT	TCT	819
Ile	Ser	Thr	Lys	Asn	Leu	Ser	Leu	Lys	Asn	Ser	Thr	Gly	Ser	Ile	Ser	
		175					180					185				
TTT	GAA	GGG	AAT	AAA	TCG	AGC	GCA	ACA	GGG	AAA	AAA	GGT	GGG	GCT	ATT	867
Phe	Glu	Gly	Asn	Lys	Ser	Ser	Ala	Thr	Gly	Lys	Lys	Gly	Gly	Ala	Ile	
	190						195					200				
TGT	GCT	ACT	GGT	ACT	GTA	GAT	ATT	ACA	AAT	AAT	ACG	GCT	CCT	ACC	CTC	915
Cys	Ala	Thr	Gly	Thr	Val	Asp	Ile	Thr	Asn	Asn	Thr	Ala	Pro	Thr	Leu	
	205					210					215					
TTC	TCG	AAC	AAT	ATT	GCT	GAA	GCT	GCA	GGT	GGA	GCT	ATA	AAT	AGC	ACA	963
Phe	Ser	Asn	Asn	Ile	Ala	Glu	Ala	Ala	Gly	Gly	Ala	Ile	Asn	Ser	Thr	
220					225				230					235		
GGA	AAC	TGT	ACA	ATT	ACA	GGG	AAT	ACG	TCT	CTT	GTA	TTT	TCT	GAA	AAT	1011

Gly	Asn	Cys	Thr	Ile	Thr	Gly	Asn	Thr	Ser	Leu	Val	Phe	Ser	Glu	Asn	
				240					245					250		
AGT	GTG	ACA	GCG	ACC	GCA	GGA	AAT	GGA	GGA	GCT	CTT	TCT	GGA	GAT	GCC	1059
Ser	Val	Thr	Ala	Thr	Ala	Gly	Asn	Gly	Gly	Ala	Leu	Ser	Gly	Asp	Ala	
			255					260					265			
GAT	GTT	ACC	ATA	TCT	GGG	AAT	CAG	AGT	GTA	ACT	TTC	TCA	GGA	AAC	CAA	1107
Asp	Val	Thr	Ile	Ser	Gly	Asn	Gln	Ser	Val	Thr	Phe	Ser	Gly	Asn	Gln	
			270				275					280				
GCT	GTA	GCT	AAT	GGC	GGA	GCC	ATT	TAT	GCT	AAG	AAG	CTT	ACA	CTG	GCT	1155
Ala	Val	Ala	Asn	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Thr	Leu	Ala	
	285					290					295					
TCC	GGG	GGG	GGG	GGG	GGT	ATC	TCC	TTT	TCT	AAC	AAT	ATA	GTC	CAA	GGT	1203
Ser	Gly	Gly	Gly	Gly	Gly	Ile	Ser	Phe	Ser	Asn	Asn	Ile	Val	Gln	Gly	
300					305					310				315		
ACC	ACT	GCA	GGT	AAT	GGT	GGA	GCC	ATT	TCT	ATA	CTG	GCA	GCT	GGA	GAG	1251
Thr	Thr	Ala	Gly	Asn	Gly	Gly	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Gly	Glu	
				320				325						330		
TGT	AGT	CTT	TCA	GCA	GAA	GCA	GGG	GAC	ATT	ACC	TTC	AAT	GGG	AAT	GCC	1299
Cys	Ser	Leu	Ser	Ala	Glu	Ala	Gly	Asp	Ile	Thr	Phe	Asn	Gly	Asn	Ala	
			335					340					345			
ATT	GTT	GCA	ACT	ACA	CCA	CAA	ACT	ACA	AAA	AGA	AAT	TCT	ATT	GAC	ATA	1347
Ile	Val	Ala	Thr	Thr	Pro	Gln	Thr	Thr	Lys	Arg	Asn	Ser	Ile	Asp	Ile	
		350					355					360				
GGA	TCT	ACT	GCA	AAG	ATC	ACG	AAT	TTA	CGT	GCA	ATA	TCT	GGG	CAT	AGC	1395
Gly	Ser	Thr	Ala	Lys	Ile	Thr	Asn	Leu	Arg	Ala	Ile	Ser	Gly	His	Ser	
	365					370				375						
ATC	TTT	TTC	TAC	GAT	CCG	ATT	ACT	GCT	AAT	ACG	GCT	GCG	GAT	TCT	ACA	1443
Ile	Phe	Phe	Tyr	Asp	Pro	Ile	Thr	Ala	Asn	Thr	Ala	Ala	Asp	Ser	Thr	
380					385				390					395		
GAT	ACT	TTA	AAT	CTC	AAT	AAG	GCT	GAT	GCA	GGT	AAT	AGT	ACA	GAT	TAT	1491
Asp	Thr	Leu	Asn	Leu	Asn	Lys	Ala	Asp	Ala	Gly	Asn	Ser	Thr	Asp	Tyr	
			400					405						410		
AGT	GGG	TCG	ATT	GTT	TTT	TCT	GGT	GAA	AAG	CTC	TCT	GAA	GAT	GAA	GCA	1539
Ser	Gly	Ser	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Ser	Glu	Asp	Glu	Ala	
			415					420					425			
AAA	GTT	GCA	GAC	AAC	CTC	ACT	TCT	ACG	CTG	AAG	CAG	CCT	GTA	ACT	CTA	1587
Lys	Val	Ala	Asp	Asn	Leu	Thr	Ser	Thr	Leu	Lys	Gln	Pro	Val	Thr	Leu	
		430					435					440				
ACT	GCA	GGA	AAT	TTA	GTA	CTT	AAA	CGT	GGT	GTC	ACT	CTC	GAT	ACG	AAA	1635
Thr	Ala	Gly	Asn	Leu	Val	Leu	Lys	Arg	Gly	Val	Thr	Leu	Asp	Thr	Lys	
	445					450				455						
GGC	TTT	ACT	CAG	ACC	GCG	GGT	TCC	TCT	GTT	ATT	ATG	GAT	GCG	GGC	ACA	1683
Gly	Phe	Thr	Gln	Thr	Ala	Gly	Ser	Ser	Val	Ile	Met	Asp	Ala	Gly	Thr	

460	465	470	475	
ACG TTA AAA GCA AGT ACA GAG GAG GTC ACT TTA ACA GGT CTT TCC ATT	Thr Leu Lys Ala Ser Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile	1731		
	480 485 490			
CCT GTA GAC TCT TTA GGC GAG GGT AAG AAA GTT GTA ATT GCT GCT TCT	Pro Val Asp Ser Leu Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser	1779		
	495 500 505			
GCA GCA AGT AAA AAT GTA GCC CTT AGT GGT CCG ATT CTT CTT TTG GAT	Ala Ala Ser Lys Asn Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp	1827		
	510 515 520			
AAC CAA GGG AAT GCT TAT GAA AAT CAC GAC TTA GGA AAA ACT CAA GAC	Asn Gln Gly Asn Ala Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp	1875		
	525 530 535			
TTT TCA TTT GTG CAG CTC TCT GCT CTG GGT ACT GCA ACA ACT ACA GAT	Phe Ser Phe Val Gln Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp	1923		
	540 545 550 555			
GTT CCA GCG GTT CCT ACA GTA GCA ACT CCT ACG CAC TAT GGG TAT CAA	Val Pro Ala Val Pro Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln	1971		
	560 565 570			
GGT ACT TGG GGA ATG ACT TGG GTT GAT GAT ACC GCA AGC ACT CCA AAG	Gly Thr Trp Gly Met Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys	2019		
	575 580 585			
ACT AAG ACA GCG ACA TTA GCT TGG ACC AAT ACA GGC TAC CTT CCG AAT	Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn	2067		
	590 595 600			
CCT GAG CGT CAA GGA CCT TTA GTT CCT AAT AGC CTT TGG GGA TCT TTT	Pro Glu Arg Gln Gly Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe	2115		
	605 610 615			
TCA GAC ATC CAA GCG ATT CAA GGT GTC ATA GAG AGA AGT GCT TTG ACT	Ser Asp Ile Gln Ala Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr	2163		
	620 625 630 635			
CTT TGT TCA GAT CGA GGC TTC TGG GCT GCG GGA GTC GCC AAT TTC TTA	Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu	2211		
	640 645 650			
GAT AAA GAT AAG AAA GGG GAA AAA CGC AAA TAC CGT CAT AAA TCT GGT	Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly	2259		
	655 660 665			
GGA TAT GCT ATC GGA GGT GCA GCG CAA ACT TGT TCT GAA AAC TTA ATT	Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile	2307		
	670 675 680			
AGC TTT GCC TTT TGC CAA CTC TTT GGT AGC GAT AAA GAT TTC TTA GTC	Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val	2355		
	685 690 695			

GCT AAA AAT CAT ACT GAT ACC TAT GCA GGA GCC TTC TAT ATC CAA CAC	2403
Ala Lys Asn His Thr Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His	
700 705 710 715	
ATT ACA GAA TGT AGT GGG TTC ATA GGT TGT CTC TTA GAT AAA CTT CCT	2451
Ile Thr Glu Cys Ser Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro	
720 725 730	
GGC TCT TGG AGT CAT AAA CCC CTC GTT TTA GAA GGG CAG CTC GCT TAT	2499
Gly Ser Trp Ser His Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr	
735 740 745	
AGC CAC GTC AGT AAT GAT CTG AAG ACA AAG TAT ACT GCG TAT CCT GAG	2547
Ser His Val Ser Asn Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu	
750 755 760	
GTG AAA GGT TCT TGG GGG AAT AAT GCT TTT AAC ATG ATG TTG GGA GCT	2595
Val Lys Gly Ser Trp Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala	
765 770 775	
TCT TCT CAT TCT TAT CCT GAA TAC CTG CAT TGT TTT GAT ACC TAT GCT	2643
Ser Ser His Ser Tyr Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala	
780 785 790 795	
CCA TAC ATC AAA CTG AAT CTG ACC TAT ATA CGT CAG GAC AGC TTC TCG	2691
Pro Tyr Ile Lys Leu Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser	
800 805 810	
GAG AAA GGT ACA GAA GGA AGA TCT TTT GAT GAC AGC AAC CTC TTC AAT	2739
Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn	
815 820 825	
TTA TCT TTG CCT ATA GGG GTG AAG TTT GAG AAG TTC TCT GAT TGT AAT	2787
Leu Ser Leu Pro Ile Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn	
830 835 840	
GAC TTT TCT TAT GAT CTG ACT TTA TCC TAT GTT CCT GAT CTT ATC CGC	2835
Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg	
845 850 855	
AAT GAT CCC AAA TGC ACT ACA GCA CTT GTA ATC AGC GGA GCC TCT TGG	2883
Asn Asp Pro Lys Cys Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp	
860 865 870 875	
GAA ACT TAT GCC AAT AAC TTA GCA CGA CAG GCC TTG CAA GTG CGT GCA	2931
Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala	
880 885 890	
GGC AGT CAC TAC GCC TTC TCT CCT ATG TTT GAA GTG CTC GGC CAG TTT	2979
Gly Ser His Tyr Ala Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe	
895 900 905	
GTC TTT GAA GTT CGT GGA TCC	3000
Val Phe Glu Val Arg Gly Ser	
910	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 914 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys
 1           5           10           15
Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly
      20           25           30
Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro
      35           40           45
Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr
      50           55           60
Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser
65           70           75           80
Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser
      85           90           95
Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr
      100          105          110
Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu
      115          120          125
Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val
      130          135          140
Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe
145          150          155          160
Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn
      165          170          175
Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys
      180          185          190
Ser Ser Ala Thr Gly Lys Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr
      195          200          205
Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile
      210          215          220
Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile
225          230          235          240
Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr
      245          250          255
Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser
      260          265          270
Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly
      275          280          285
Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly Gly
      290          295          300
Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn
305          310          315          320
Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser Leu Ser Ala
      325          330          335
Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val Ala Thr Thr
      340          345          350

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Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser Thr Ala Lys
 355 360 365
 Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380
 Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400
 Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415
 Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430
 Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445
 Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460
 Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480
 Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495
 Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510
 Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525
 Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540
 Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560
 Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575
 Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590
 Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly
 595 600 605
 Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala
 610 615 620
 Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg
 625 630 635 640
 Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys
 645 650 655
 Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly
 660 665 670
 Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys
 675 680 685
 Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr
 690 695 700
 Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser
 705 710 715 720
 Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His
 725 730 735
 Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn
 740 745 750
 Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp
 755 760 765
 Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr
 770 775 780
 Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu
 785 790 795 800
 Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu

				805				810				815			
Gly	Arg	Ser	Phe	Asp	Asp	Ser	Asn	Leu	Phe	Asn	Leu	Ser	Leu	Pro	Ile
				820				825				830			
Gly	Val	Lys	Phe	Glu	Lys	Phe	Ser	Asp	Cys	Asn	Asp	Phe	Ser	Tyr	Asp
				835				840				845			
Leu	Thr	Leu	Ser	Tyr	Val	Pro	Asp	Leu	Ile	Arg	Asn	Asp	Pro	Lys	Cys
				850				855				860			
Thr	Thr	Ala	Leu	Val	Ile	Ser	Gly	Ala	Ser	Trp	Glu	Thr	Tyr	Ala	Asn
				865				870				875			
Asn	Leu	Ala	Arg	Gln	Ala	Leu	Gln	Val	Arg	Ala	Gly	Ser	His	Tyr	Ala
				885				890				895			
Phe	Ser	Pro	Met	Phe	Glu	Val	Leu	Gly	Gln	Phe	Val	Phe	Glu	Val	Arg
				900				905				910			
Gly	Ser														

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1200
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAT Asp 1	CCT Pro	AAA Lys	AAT Asn	AAA Lys 5	GAG Glu	TAC Tyr	ACA Thr	GGG Gly	ACC Thr 10	ATA Ile	CTC Leu	TTT Phe	TCT Ser	GGA Gly 15	GAA Glu	48
AAG Lys	AGT Ser	CTA Leu	GCA Ala 20	AAC Asn	GAT Asp	CCT Pro	AGG Arg	GAT Asp 25	TTT Phe	AAA Lys	TCT Ser	ACA Thr	ATC Ile 30	CCT Pro	CAG Gln	96
AAC Asn	GTC Val	AAC Asn 35	CTG Leu	TCT Ser	GCA Ala	GGA Gly	TAC Tyr 40	TTA Leu	GTT Val	ATT Ile	AAA Lys	GAG Glu 45	GGG Gly	GCC Ala	GAA Glu	144
GTC Val 50	ACA Thr	GTT Val	TCA Ser	AAA Lys	TTC Phe	ACG Thr 55	CAG Gln	TCT Ser	CCA Pro	GGA Gly	TCG Ser 60	CAT His	TTA Leu	GTT Val	TTA Leu	192
GAT Asp 65	TTA Leu	GGA Gly	ACC Thr	AAA Lys 70	CTG Leu 75	ATA Ile	GCC Ala	TCT Ser	AAG Lys	GAA Glu 80	GAC Asp	ATT Ile	GCC Ala	ATC Ile	ACA Thr	240
GGC Gly	CTC Leu	GCG Ala	ATA Ile	GAT Asp 85	ATA Ile	GAT Asp	AGC Ser	TTA Leu	AGC Ser	TCA Ser	TCC Ser	TCA Ser	ACA Thr	GCA Ala 95	GCT Ala	288

GTT	ATT	AAA	GCA	AAC	ACC	GCA	AAT	AAA	CAG	ATA	TCC	GTG	ACG	GAC	TCT	336
Val	Ile	Lys	Ala	Asn	Thr	Ala	Asn	Lys	Gln	Ile	Ser	Val	Thr	Asp	Ser	
		100						105					110			
ATA	GAA	CTT	ATC	TCG	CCT	ACT	GGC	AAT	GCC	TAT	GAA	GAT	CTC	AGA	ATG	384
Ile	Glu	Leu	Ile	Ser	Pro	Thr	Gly	Asn	Ala	Tyr	Glu	Asp	Leu	Arg	Met	
		115					120					125				
AGA	AAT	TCA	CAG	ACG	TTC	CCT	CTG	CTC	TCT	TTA	GAG	CCT	GGA	GCC	GGG	432
Arg	Asn	Ser	Gln	Thr	Phe	Pro	Leu	Leu	Ser	Leu	Glu	Pro	Gly	Ala	Gly	
	130					135					140					
GGT	AGT	GTG	ACT	GTA	ACT	GCT	GGA	GAT	TTC	CTA	CCG	GTA	AGT	CCC	CAT	480
Gly	Ser	Val	Thr	Val	Thr	Ala	Gly	Asp	Phe	Leu	Pro	Val	Ser	Pro	His	
145					150					155					160	
TAT	GGT	TTT	CAA	GGC	AAT	TGG	AAA	TTA	GCT	TGG	ACA	GGA	ACT	GGA	AAC	528
Tyr	Gly	Phe	Gln	Gly	Asn	Trp	Lys	Leu	Ala	Trp	Thr	Gly	Thr	Gly	Asn	
			165					170						175		
AAA	GTT	GGA	GAA	TTC	TTC	TGG	GAT	AAA	ATA	AAT	TAT	AAG	CCT	AGA	CCT	576
Lys	Val	Gly	Glu	Phe	Phe	Trp	Asp	Lys	Ile	Asn	Tyr	Lys	Pro	Arg	Pro	
		180						185					190			
GAA	AAA	GAA	GGA	AAT	TTA	GTT	CCT	AAT	ATC	TTG	TGG	GGG	AAT	GCT	GTA	624
Glu	Lys	Glu	Gly	Asn	Leu	Val	Pro	Asn	Ile	Leu	Trp	Gly	Asn	Ala	Val	
		195					200					205				
AAT	GTC	AGA	TCC	TTA	ATG	CAG	GTT	CAA	GAG	ACC	CAT	GCA	TCG	AGC	TTA	672
Asn	Val	Arg	Ser	Leu	Met	Gln	Val	Gln	Glu	Thr	His	Ala	Ser	Ser	Leu	
	210					215					220					
CAG	ACA	GAT	CGA	GGG	CTG	TGG	ATC	GAT	GGA	ATT	GGG	AAT	TTC	TTC	CAT	720
Gln	Thr	Asp	Arg	Gly	Leu	Trp	Ile	Asp	Gly	Ile	Gly	Asn	Phe	Phe	His	
225					230				235						240	
GTA	TCT	GCC	TCC	GAA	GAC	AAT	ATA	AGG	TAC	CGT	CAT	AAC	AGC	GGT	GGA	768
Val	Ser	Ala	Ser	Glu	Asp	Asn	Ile	Arg	Tyr	Arg	His	Asn	Ser	Gly	Gly	
				245				250						255		
TAT	GTT	CTA	TCT	GTA	AAT	AAT	GAG	ATC	ACA	CCT	AAG	CAC	TAT	ACT	TCG	816
Tyr	Val	Leu	Ser	Val	Asn	Asn	Glu	Ile	Thr	Pro	Lys	His	Tyr	Thr	Ser	
		260					265						270			
ATG	GCA	TTT	TCC	CAA	CTC	TTT	AGT	AGA	GAC	AAA	GAC	TAT	GCG	GTT	TCC	864
Met	Ala	Phe	Ser	Gln	Leu	Phe	Ser	Arg	Asp	Lys	Asp	Tyr	Ala	Val	Ser	
		275					280					285				
AAC	AAC	GAA	TAC	AGA	ATG	TAT	TTA	GGA	TCG	TAT	CTC	TAT	CAA	TAT	ACA	912
Asn	Asn	Glu	Tyr	Arg	Met	Tyr	Leu	Gly	Ser	Tyr	Leu	Tyr	Gln	Tyr	Thr	
		290				295					300					
ACC	TCC	CTA	GGG	AAT	ATT	TTC	CGT	TAT	GCT	TCG	CGT	AAC	CCT	AAT	GTA	960
Thr	Ser	Leu	Gly	Asn	Ile	Phe	Arg	Tyr	Ala	Ser	Arg	Asn	Pro	Asn	Val	
305					310				315						320	
AAC	GTC	GGG	ATT	CTC	TCA	AGA	AGG	TTT	CTT	CAA	AAT	CCT	CTT	ATG	ATT	1008

Asn Val Gly Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile	
325 330 335	
TTT CAT TTT TTG TGT GCT TAT GGT CAT GCC ACC AAT GAT ATG AAA ACA	1056
Phe His Phe Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr	
340 345 350	
GAC TAC GCA AAT TTC CCT ATG GTG AAA AAC AGC TGG AGA AAC AAT TGT	1104
Asp Tyr Ala Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys	
355 360 365	
TGG GCT ATA AAA TGC GGA GGG AGC ATG CCT CTA TTG GTA TTT GAA AAC	1152
Trp Ala Ile Lys Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn	
370 375 380	
GGA AAA CTT TTC CAA GGT GCC ATC CCA TTT ATG AAA CTA CAA TTA GTT	1200
Gly Lys Leu Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val	
385 390 395 400	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu	
1 5 10 15	
Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln	
20 25 30	
Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu	
35 40 45	
Val Thr Val Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu	
50 55 60	
Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr	
65 70 75 80	
Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Thr Ala Ala	
85 90 95	
Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser	
100 105 110	
Ile Glu Leu Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met	
115 120 125	
Arg Asn Ser Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly	
130 135 140	
Gly Ser Val Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His	
145 150 155 160	
Tyr Gly Phe Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn	
165 170 175	
Lys Val Gly Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro	
180 185 190	

Glu Lys Glu Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val
 195 200 205
 Asn Val Arg Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu
 210 215 220
 Gln Thr Asp Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His
 225 230 235 240
 Val Ser Ala Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly
 245 250 255
 Tyr Val Leu Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser
 260 265 270
 Met Ala Phe Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser
 275 280 285
 Asn Asn Glu Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr
 290 295 300
 Thr Ser Leu Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val
 305 310 315 320
 Asn Val Gly Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile
 325 330 335
 Phe His Phe Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr
 340 345 350
 Asp Tyr Ala Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys
 355 360 365
 Trp Ala Ile Lys Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn
 370 375 380
 Gly Lys Leu Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1830
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAT CTC ACA TTA GGG AGT CGT GAC AGT TAT AAT GGT GAT ACA AGC ACC 48
 Asp Leu Thr Leu Gly Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr
 1 5 10 15
 ACA GAA TTT ACT CCT AAA GCG GCA ACT TCT GAT GCT AGT GGC ACG ACC 96
 Thr Glu Phe Thr Pro Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr
 20 25 30
 TAT ATT CTC GAT GGG GAT GTC TCG ATA AGC CAA GCA GGG AAA CAA ACG 144
 Tyr Ile Leu Asp Gly Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr
 35 40 45

AGC	TTA	ACC	ACA	AGT	TGT	TTT	TCT	AAC	ACT	GCA	GGA	AAT	CTT	ACC	TTC	192
Ser	Leu	Thr	Thr	Ser	Cys	Phe	Ser	Asn	Thr	Ala	Gly	Asn	Leu	Thr	Phe	
50						55					60					
TTA	GGG	AAC	GGA	TTT	TCT	CTT	CAT	TTT	GAC	AAT	ATT	ATT	TCG	TCT	ACT	240
Leu	Gly	Asn	Gly	Phe	Ser	Leu	His	Phe	Asp	Asn	Ile	Ile	Ser	Ser	Thr	
65					70				75						80	
GTT	GCA	GGT	GTT	GTT	GTT	AGC	AAT	ACA	GCA	GCT	TCT	GGG	ATT	ACG	AAA	288
Val	Ala	Gly	Val	Val	Val	Ser	Asn	Thr	Ala	Ala	Ser	Gly	Ile	Thr	Lys	
				85					90						95	
TTC	TCA	GGA	TTT	TCA	ACT	CTT	CGG	ATG	CTT	GCA	GCT	CCT	AGG	ACC	ACA	336
Phe	Ser	Gly	Phe	Ser	Thr	Leu	Arg	Met	Leu	Ala	Ala	Pro	Arg	Thr	Thr	
			100					105						110		
GGT	AAA	GGA	GCC	ATT	AAA	ATT	ACC	GAT	GGT	CTG	GTG	TTT	GAG	AGT	ATA	384
Gly	Lys	Gly	Ala	Ile	Lys	Ile	Thr	Asp	Gly	Leu	Val	Phe	Glu	Ser	Ile	
	115						120						125			
GGG	AAT	CTT	GAT	CCG	ATT	ACT	GTA	ACA	GGA	TCG	ACA	TCT	GTT	GCT	GAT	432
Gly	Asn	Leu	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp	
	130					135					140					
GCT	CTC	AAT	ATT	AAT	AGC	CCT	GAT	ACT	GGA	GAT	AAC	AAA	GAG	TAT	ACG	480
Ala	Leu	Asn	Ile	Asn	Ser	Pro	Asp	Thr	Gly	Asp	Asn	Lys	Glu	Tyr	Thr	
145					150					155					160	
GGA	ACC	ATA	GTC	TTT	TCT	GGA	GAG	AAG	CTC	ACG	GAG	GCA	GAA	GCT	AAA	528
Gly	Thr	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Thr	Glu	Ala	Glu	Ala	Lys	
			165						170					175		
GAT	GAG	AAG	AAC	CGC	ACT	TCT	AAA	TTA	CTT	CAA	AAT	GTT	GCT	TTT	AAA	576
Asp	Glu	Lys	Asn	Arg	Thr	Ser	Lys	Leu	Leu	Gln	Asn	Val	Ala	Phe	Lys	
			180					185					190			
AAT	GGG	ACT	GTA	GTT	TTA	AAA	GGT	GAT	GTC	GTT	TTA	AGT	GCG	AAC	GGT	624
Asn	Gly	Thr	Val	Val	Leu	Lys	Gly	Asp	Val	Val	Leu	Ser	Ala	Asn	Gly	
	195						200					205				
TTC	TCT	CAG	GAT	GCA	AAC	TCT	AAG	TTG	ATT	ATG	GAT	TTA	GGG	ACG	TCG	672
Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser	
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ATA	GAC	TCT	CTC	AGG	AAC	GGG	AAA	AAG	ATA	AAA	CTC	AGT	GCT	GCC	ACA	768
Ile	Asp	Ser	Leu	Arg	Asn	Gly	Lys	Lys	Ile	Lys	Leu	Ser	Ala	Ala	Thr	
			245						250					255		
GCT	CAG	AAA	GAT	ATT	CGT	ATA	GAT	CGT	CCT	GTT	GTA	CTG	GCA	ATT	AGC	816
Ala	Gln	Lys	Asp	Ile	Arg	Ile	Asp	Arg	Pro	Val	Val	Leu	Ala	Ile	Ser	
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Asp	Ser	Arg	Ser	Ile	Asp	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly	
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AAG	TGG	ACG	ATC	AAT	TGG	TCT	ACT	GAT	GAT	AAG	AAA	GCT	ACG	GTT	TCT	1008
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Gly	His	Thr	Asp	His	Arg	Met	Lys	Thr	Glu	Ser	Leu	Pro	Pro	Pro	Pro	

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Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala			
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Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly			
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Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser			
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CGC CAA GAT AGC TTT GTT GAA CTA GGA GCT ATC AGT CGT GAT TTT AGT			1728
Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser			
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GAT TCG CAT CTT TAT AAC CTT GCG ATT CCT CTT GGA ATC AAG TTA GAG			1776
Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu			
580	585	590	
AAA CGG TTT GCA GAG CAA TAT TAT CAT GTT GTT GCG ATG TAT TCT CCA			1824
Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro			
595	600	605	
GAT GTT			1830
Asp Val			
610			

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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Tyr Ile Leu Asp Gly Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr
          35          40          45
Ser Leu Thr Thr Ser Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe
          50          55          60
Leu Gly Asn Gly Phe Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr
65          70          75          80
Val Ala Gly Val Val Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys
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Phe Ser Gly Phe Ser Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr

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Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser													
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Leu	Val	Ala	Asn	Thr	Glu	Ser	Ile	Glu	Leu	Thr	Asn	Leu	Glu	Ile	Asn													
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Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser													
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Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu													
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										420			425			430												
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[illegible]

Claims

1. Species specific diagnostic test for identifying infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said test comprising detecting in a patient or in
5 a patient sample the presence of antibodies against one or more proteins from the outer membrane of *Chlamydia pneumoniae*, said proteins being of a molecular weight of 100.3-89.6 kDa or of 56.1 kDa, or detecting the presence of nucleic acid fragments encoding said outer membrane proteins.
- 10 2. Diagnostic test according to claim 1, wherein the outer membrane protein has the sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or in SEQ ID NO: 24, or a variant
15 or subsequence thereof.
3. Diagnostic test according to claim 1, wherein the nucleic acid fragment has the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO:
20 19, SEQ ID NO: 21, or in SEQ ID NO: 23, or a variant or subsequence thereof.
4. Diagnostic test according to claim 3 wherein detection of nucleic acid fragments is obtained by using nucleic acid amplification.
- 25 5. Diagnostic test according to claim 4, wherein detection of nucleic acid fragments is obtained by using polymerase chain reaction.
6. A nucleic acid fragment derived from *Chlamydia pneumoniae* comprising the nucleotide sequence SEQ ID NO: 1, SEQ ID NO:
30 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, or SEQ ID NO: 23, or a variant or subsequence thereof.

of said nucleotide sequence which has a sequence homology of at least 50% with any of the sequences mentioned.

7. A protein derived from *Chlamydia pneumoniae* having the amino acid sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a variant or subsequence thereof having a sequence similarity of at least 50% and a similar biological function.
8. Polyclonal monospecific antibody against the protein with the sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a variant or subsequence thereof.
9. A diagnostic kit for the diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said kit comprising a protein with the amino acid sequence SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a variant or subsequence thereof.
10. A diagnostic kit for the diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said kit comprising antibodies against a protein with the amino acid sequence SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a variant or subsequence thereof.
11. A diagnostic kit for the diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*, said kit comprising a nucleic acid fragment with the sequence SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO:

17, SEQ ID NO: 19, SEQ ID NO: 21, or SEQ ID NO: 23, or a variant or subsequence thereof.

12. A composition for immunizing a mammal, such as a human, against *Chlamydia pneumoniae*, said composition

5 comprising a protein with the amino acid sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a variant or subsequence thereof.

10 13. Use of a protein with the sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a variant or subsequence thereof in diagnosis of infection of a
15 mammal, such as a human, with *Chlamydia pneumoniae*.

14. Use of the protein with the sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24 or a
20 variant or subsequence thereof in an undenatured form, in diagnosis of infection of a mammal, such as a human, with *Chlamydia pneumoniae*.

15. Use of a protein with the sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a
25 variant or subsequence thereof, for immunizing a mammal, such as a human, against *Chlamydia pneumoniae*.

16. Use of the protein with the sequence shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, or SEQ ID NO: 24, or a
30 variant or subsequence thereof in an undenatured form, for

immunizing a mammal, such as a human, against *Chlamydia pneumoniae*.

17. Use of a nucleic acid fragment with the nucleotide sequence shown in SEQ ID NO: 1 SEQ ID NO: 3, SEQ ID NO: 5, 5 SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, or SEQ ID NO: 23, or a variant or subsequence of said nucleotide sequence which has a sequence homology of at least 50% with 10 as a human, against *Chlamydia pneumoniae*.

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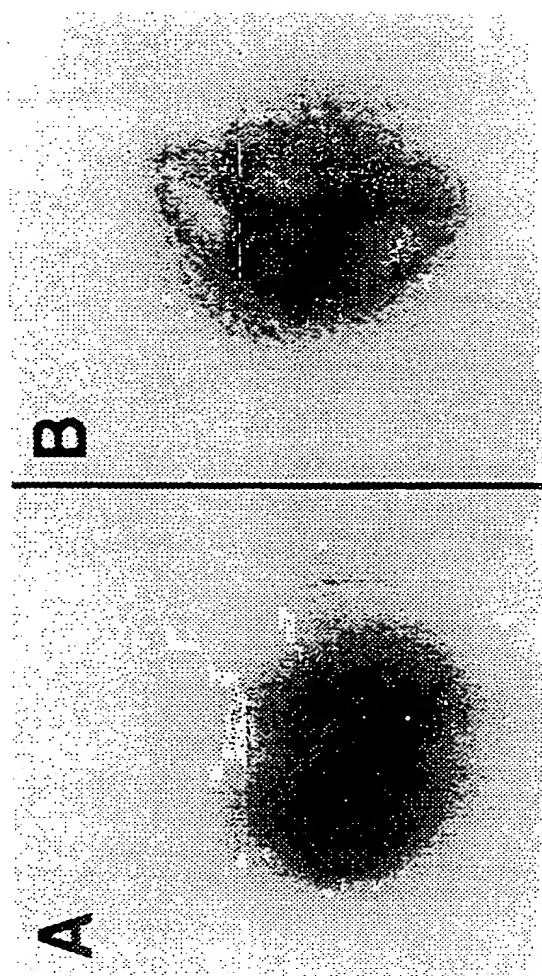


Fig. 1

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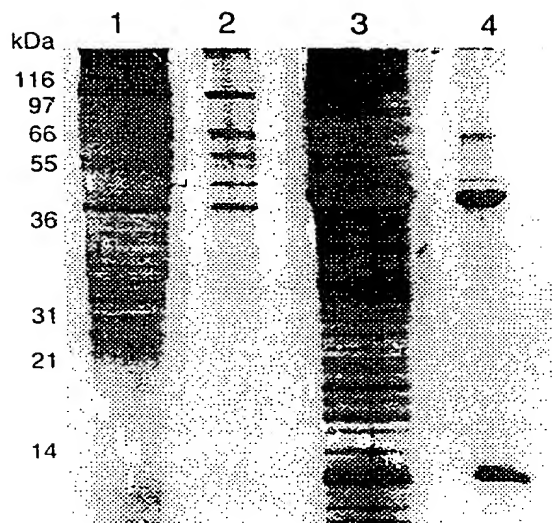


Fig. 2

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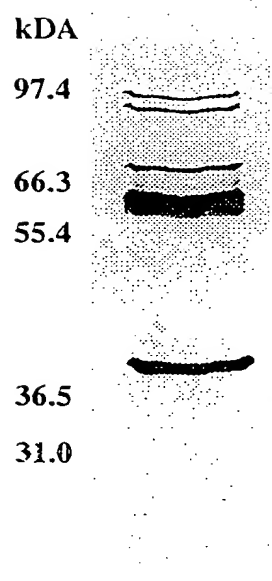


Fig. 3

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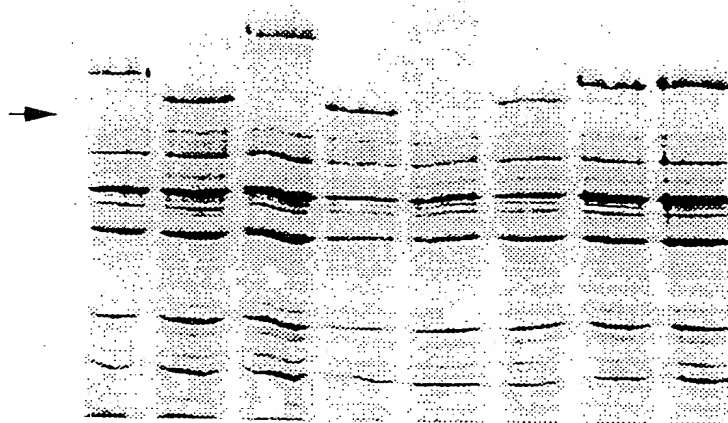


Fig. 4

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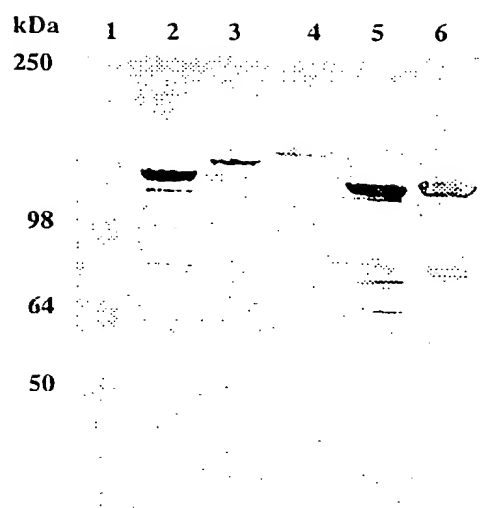


Fig. 5

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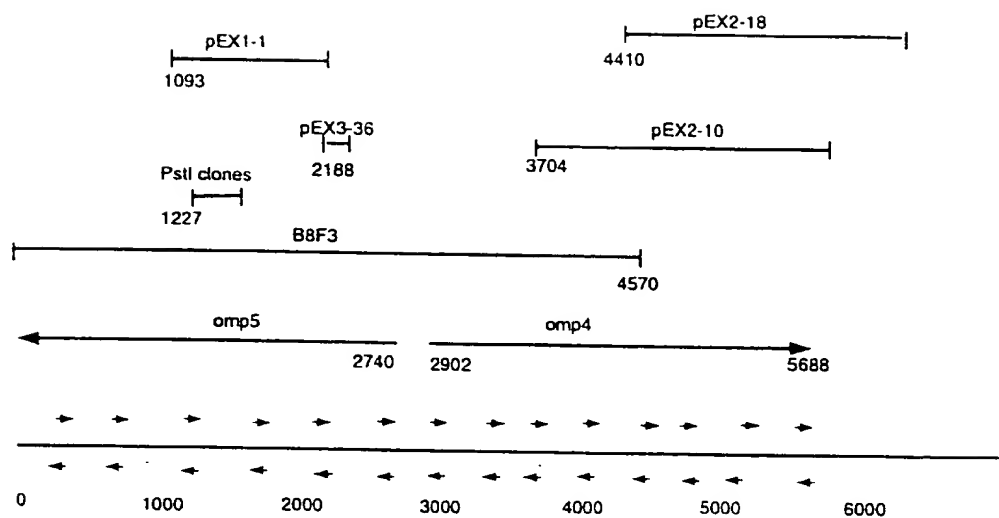


Fig. 6

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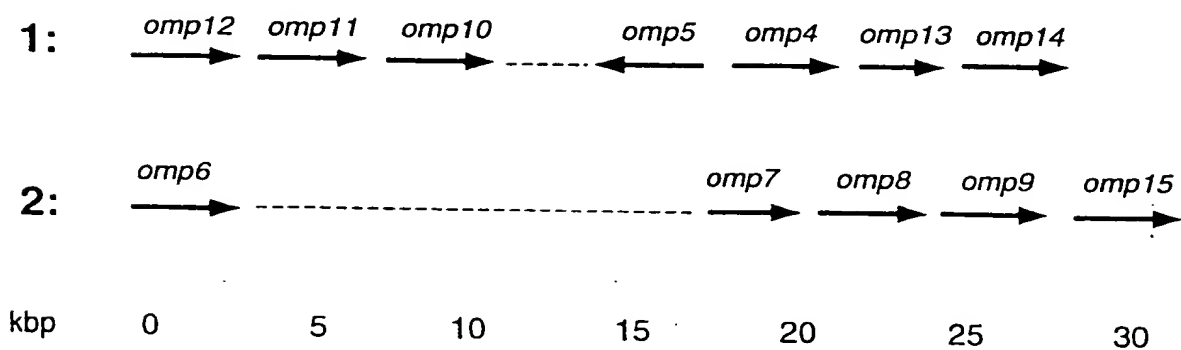
C. pneumoniae omp4-15 gene clusters

Fig. 7

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[illegible]

Fig. 8B

[illegible]

Fig. 8D

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0
500
497
494
499
497
487
514
405
487
396
262

omp12  L S L K H G V T L Q T K A F T Q Q Q A G S S R L E M D V G T T L L K E P - A D T S T I N N G L V I I N I S S I D
omp8   L V L K R G V T L D T K G I F T Q Q Q A G S S R L E M D V G T T L L K E P - A D T S T I N N G L V I I N I S S I D
omp5   L V L K R G V T L D T K G I F T Q Q Q A G S S R L E M D V G T T L L K E P - A D T S T I N N G L V I I N I S S I D
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omp6   L V L K R G V T L D T K G I F T Q Q Q A G S S R L E M D V G T T L L K E P - A D T S T I N N G L V I I N I S S I D
omp13  L V L K R G V T L D T K G I F T Q Q Q A G S S R L E M D V G T T L L K E P - A D T S T I N N G L V I I N I S S I D
omp14  L V L K R G V T L D T K G I F T Q Q Q A G S S R L E M D V G T T L L K E P - A D T S T I N N G L V I I N I S S I D

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0
548
545
542
547
545
535
562
454
536
445
262

omp12  G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp8   G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp5   G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp9   G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp11  G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp10  G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp4   G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp15  G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp7   G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp6   G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp13  G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L
omp14  G A K K G E G T G N K K E T K K A T S K K N N L T A L S S G T I T L L D P T G T N Y S Q P Q D D I L E L L

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Fig. 8F

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0      590      591      586      592      591      583      610      493      576      495      262
omp12  K A S G T V - - - - - T S T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp8   S A L G T A - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp5   S A Q G T A - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp9   T A A D P A - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp11  T A D D A D V D T I I S A D S R S - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp10  T V D A G G D I V I S A D S R S - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp4   S P G A G G D I V I S A D S R S - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp15  D A G K D I V I S A D S R S - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp7   E P G A G G D I V I S A D S R S - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp6   E L G P S F - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp13  E L G P S F - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -
omp14  E L G P S F - - - - - T T T T T T T S D I I N V D T I I S A D S R S - - - - - T A V V P P A V - - - - - T P - - - - -

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0      640      641      636      642      641      633      660      543      626      514      262
omp12  T F L A T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp8   T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp5   T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp9   T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp11  T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp10  T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp4   T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp15  T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp7   T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp6   T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp13  T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -
omp14  T L L T T M T T A N L T V S F F T P T K K K T V - - - - - T A V V P P A V - - - - - T P - - - - -

```

Fig. 8G

[illegible]

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[illegible][illegible]

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omp12	C	F	-	279
omp8	Q	F	-	928
omp5	Q	F	-	928
omp9	G	F	-	918
omp11	S	F	-	930
omp10	Q	F	-	928
omp4	R	F	-	928
omp15	R	F	-	945
omp7	K	F	-	841
omp6	R	F	-	922
omp13	-	-	-	514
omp14	-	-	-	262

Fig. 8j

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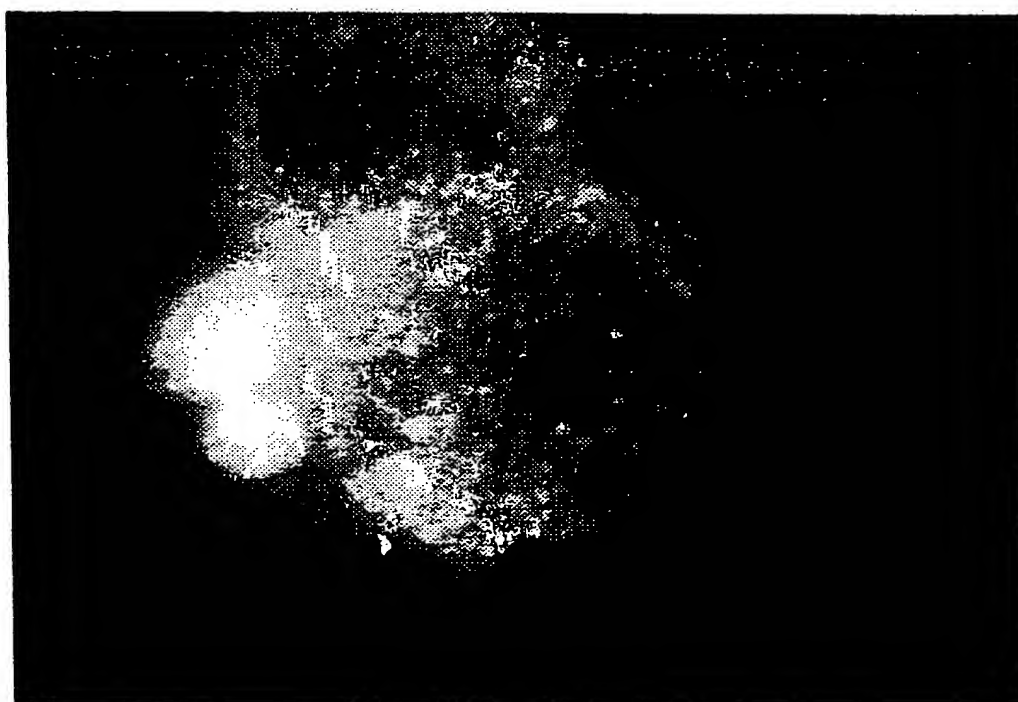
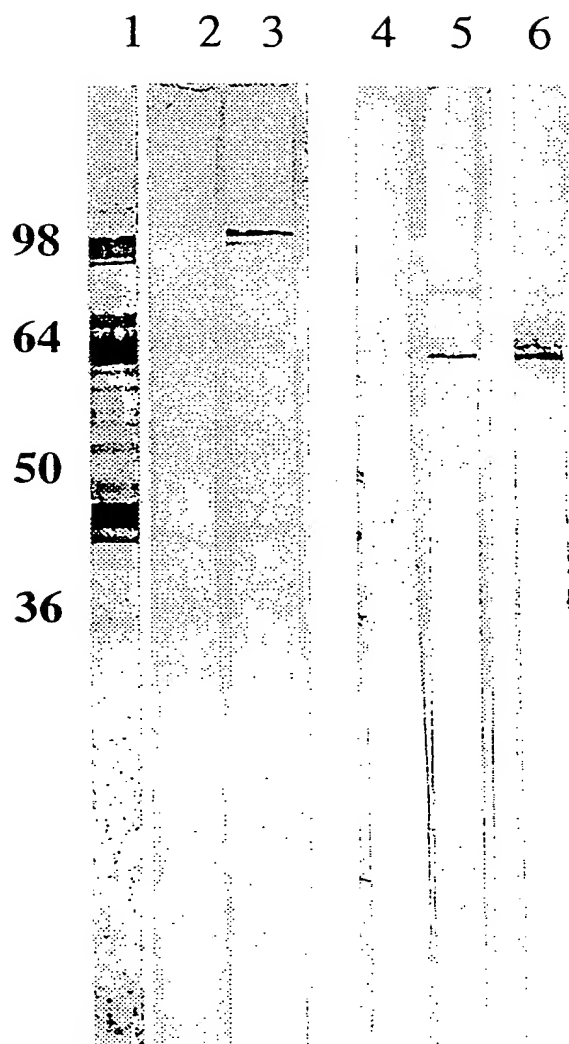


Fig. 9

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Immunoblotting of *C. pneumoniae* EB, lane 1-3 heated to 100°C in SDS-sample buffer, lane 4-6 unheated. Lane 1 reacted with rabbit anti *C. pneumoniae* OMC; lane 2 and 4 pre-serum; lane 3 and 5 polyclonal rabbit anti pEX1-1 fusion protein; lane 6 MAb 26.1.

Fig. 10

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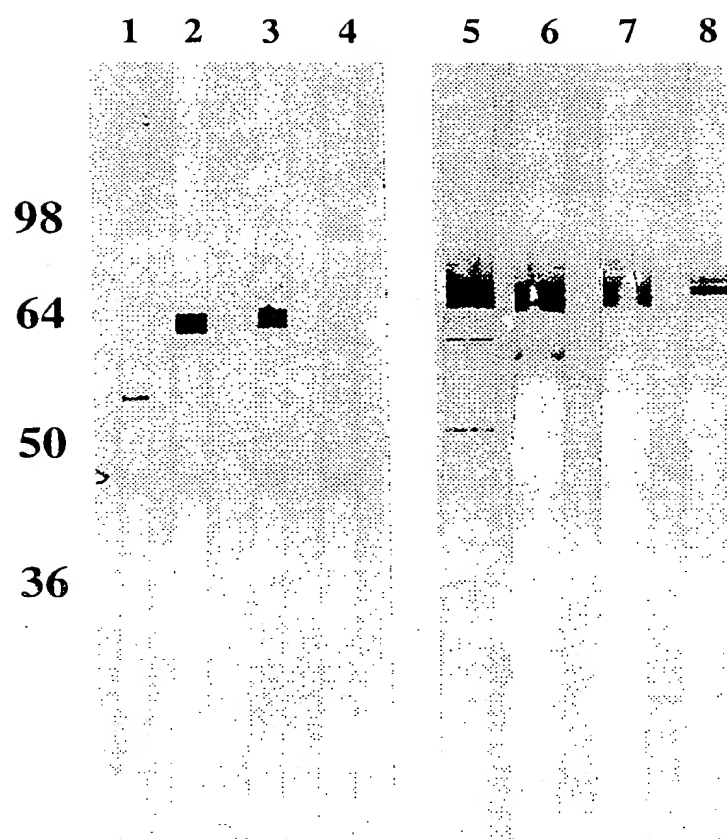


Fig. 11

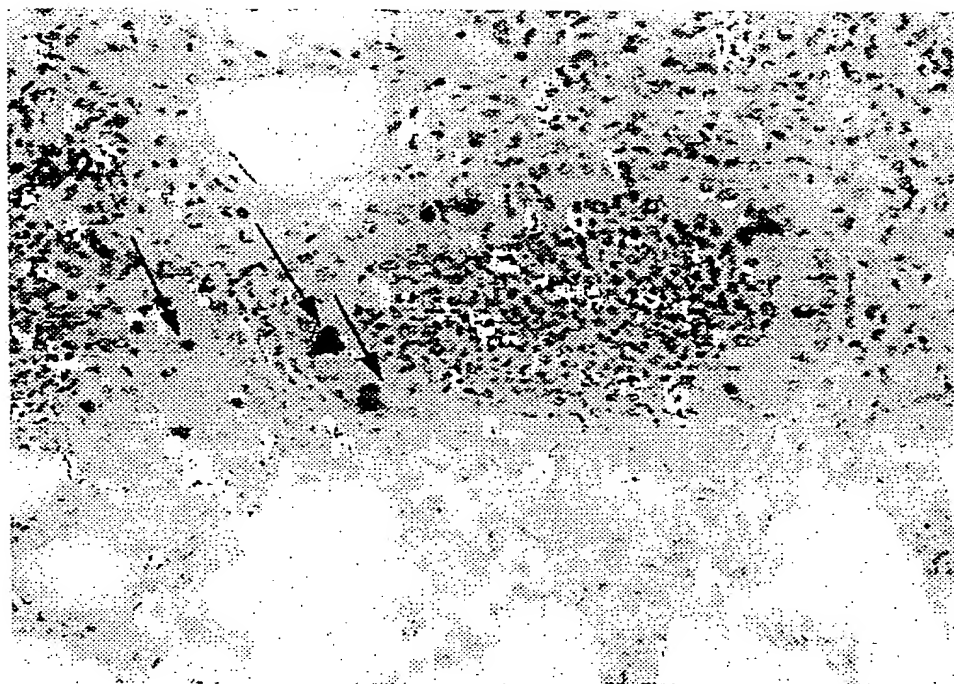


Fig. 12

